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<110> Pickard, Benjamin Simon  
Blackwood, Douglas  
Porteous, David  
Muir, Walter John  
Mors, Ole  
Ewald, Henrik Lykke

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Pro Arg Asn Tyr Ser Met Ile Val Met Phe Thr Ala Leu Gln Pro Gln
          85           90           95

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```

Arg Gln Cys Ser Val Cys Arg Gln Ala Asn Glu Glu Tyr Gln Ile Leu
          100          105          110

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Ala Asn Ser Trp Arg Tyr Ser Ser Ala Phe Cys Asn Lys Leu Phe Phe
          115          120          125

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Ser Met Val Asp Tyr Asp Glu Gly Thr Asp Val Phe Gln Gln Leu Asn  
 130 135 140

Met Asn Ser Ala Pro Thr Phe Met His Phe Pro Pro Lys Gly Arg Pro  
 145 150 155 160

Lys Arg Ala Asp Thr Phe Asp Leu Gln Arg Ile Gly Phe Ala Ala Glu  
 165 170 175

Gln Leu Ala Lys Trp Ile Ala Asp Arg Thr Asp Val His Ile Arg Val  
 180 185 190

Phe Arg Pro Pro Asn Tyr Ser Gly Thr Ile Ala Leu Ala Leu Leu Val  
 195 200 205

Ser Leu Val Gly Gly Leu Leu Tyr Leu Arg Arg Asn Asn Leu Glu Phe  
 210 215 220

Ile Tyr Asn Lys Thr Gly Trp Ala Met Val Ser Leu Cys Ile Val Phe  
 225 230 235 240

Ala Met Thr Ser Gly Gln Met Trp Asn His Ile Arg Gly Pro Pro Tyr  
 245 250 255

Ala His Lys Asn Pro His Asn Gly Gln Val Ser Tyr Ile His Gly Ser  
 260 265 270

Ser Gln Ala Gln Phe Val Ala Glu Ser His Ile Ile Leu Val Leu Asn  
 275 280 285

Ala Ala Ile Thr Met Gly Met Val Leu Leu Asn Glu Ala Ala Thr Ser  
 290 295 300

Lys Gly Asp Val Gly Lys Arg Arg Ile Ile Cys Leu Val Gly Leu Gly  
 305 310 315 320

Leu Val Val Phe Phe Phe Ser Phe Leu Leu Ser Ile Phe Arg Ser Lys  
 325 330 335

Tyr His Gly Tyr Pro Tyr Ser Asp Leu Asp Phe Glu  
 340 345

<210> 16  
 <211> 982  
 <212> DNA  
 <213> Homo sapiens

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<400> 16
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attgttatgt tcaactgctct tcagcctcag cggcagtggt ctgtgtgcag gcaagctaatt      180
gaagaatatc aaataactggc gaactcctgg cgctattcat ctgctttttg taacaagctc      240
ttcttcagta tgggtggacta tgatgagggg acagacgttt ttcagcagct caacatgaac      300
tctgctccta cattcatgca ttttcctcca aaaggcagac ctaagagagc tgatactttt      360
gacctccaaa gaattgggatt tgcagctgag caactagcaa agtggattgc tgacagaacg      420
gatgttcata ttcggggtttt cagaccaccc aactactctg gtaccattgc tttggccctg      480
ttagtgctgc ttgttggagg tttgctttat ttgagaagga acaacttggg gttcatctat      540
aacaagactg gttggggccat ggtgtctctg tgtatagtct ttgctatgac ttctggccag      600
atgtggaacc atatccgtgg acctccatat gtcataaga acccacacaa tggacaagtg      660
agctacattc atgggagcag ccaggctcag tttgtggcag aatcacacat tattctggta      720
ctgaatgccg ctatcaccat ggggatgggt cttctaaatg aagcagcaac ttcgaaaggc      780
gatgttggaa aaagacggat aatttgcta gtgggattgg gcctgggtgt cttcttcttc      840
agttttctac tttcaatatt tcgttccaag taccacgggt atccttatag ctttttaatt      900
aaatgaagcc aagtgggatt tgcataaagt gaatgtttac catgaagata aactgttcct      960
gactttatac tattttgaat tc                                          982

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<210> 17
<211> 347
<212> PRT
<213> Homo sapiens

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<400> 17

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Met Gly Ala Arg Gly Ala Pro Ser Arg Arg Arg Gln Ala Gly Arg Arg
1           5           10           15

```

```

Leu Arg Tyr Leu Pro Thr Gly Ser Phe Pro Phe Leu Leu Leu Leu Leu
20           25           30

```

```

Leu Leu Cys Ile Gln Leu Gly Gly Gly Gln Lys Lys Lys Glu Asn Leu
35           40           45

```

```

Leu Ala Glu Lys Val Glu Gln Leu Met Glu Trp Ser Ser Arg Arg Ser
50           55           60

```

```

Ile Phe Arg Met Asn Gly Asp Lys Phe Arg Lys Phe Ile Lys Ala Pro

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65		70		75		80
Pro Arg Asn Tyr Ser Met Ile Val Met Phe Thr Ala Leu Gln Pro Gln						
		85		90		95
Arg Gln Cys Ser Val Cys Arg Gln Ala Asn Glu Glu Tyr Gln Ile Leu						
		100		105		110
Ala Asn Ser Trp Arg Tyr Ser Ser Ala Phe Cys Asn Lys Leu Phe Phe						
		115		120		125
Ser Met Val Asp Tyr Asp Glu Gly Thr Asp Val Phe Gln Gln Leu Asn						
		130		135		140
Met Asn Ser Ala Pro Thr Phe Met His Phe Pro Pro Lys Gly Arg Pro						
		145		150		155
Lys Arg Ala Asp Thr Phe Asp Leu Gln Arg Ile Gly Phe Ala Ala Glu						
		165		170		175
Gln Leu Ala Lys Trp Ile Ala Asp Arg Thr Asp Val His Ile Arg Val						
		180		185		190
Phe Arg Pro Pro Asn Tyr Ser Gly Thr Ile Ala Leu Ala Leu Leu Val						
		195		200		205
Ser Leu Val Gly Gly Leu Leu Tyr Leu Arg Arg Asn Asn Leu Glu Phe						
		210		215		220
Ile Tyr Asn Lys Thr Gly Trp Ala Met Val Ser Leu Cys Ile Val Phe						
		225		230		235
Ala Met Thr Ser Gly Gln Met Trp Asn His Ile Arg Gly Pro Pro Tyr						
		245		250		255
Ala His Lys Asn Pro His Asn Gly Gln Val Ser Tyr Ile His Gly Ser						
		260		265		270
Ser Gln Ala Gln Phe Val Ala Glu Ser His Ile Ile Leu Val Leu Asn						
		275		280		285
Ala Ala Ile Thr Met Gly Met Val Leu Leu Asn Glu Ala Ala Thr Ser						
		290		295		300
Lys Gly Asp Val Gly Lys Arg Arg Ile Ile Cys Leu Val Gly Leu Gly						
		305		310		315
						320

Leu Val Val Phe Phe Phe Ser Phe Leu Leu Ser Ile Phe Arg Ser Lys  
 325 330 335

Tyr His Gly Tyr Pro Tyr Ser Phe Leu Ile Lys  
 340 345

<210> 18  
 <211> 752  
 <212> DNA  
 <213> Homo sapiens

<400> 18  
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 attgttatgt tcaactgctct tcagcctcag cggcagtgtt ctgtgtgcag gcaagctaata 180  
 gaagaatatc aaatactggc gaactcctgg cgctattcat ctgctttttg taacaagctc 240  
 ttcttcagta tgggtggacta tgatgagggg acagacgttt ttcagcagct caacatgaac 300  
 tctgctccta cattcatgca ttttctcca aaaggcagac ctaagagagc tgatactttt 360  
 gacctccaaa gaattggatt tgcagctgag caactagcaa agtggattgc tgacagaacg 420  
 gatgttcata ttcgggtttt cagaccaccc aactactctg gtaccattgc tttggccctg 480  
 ttagtgctgc ttgttggagg tttgctttat ttgagaagga acaacttgga gttcatctat 540  
 aacaagactg gttgggcat ggtgtctctg tgtatagtct ttgctatgac ttctggccag 600  
 atgtggaacc atatccgtgg acctccatat gtcataaga acccacacaa tggacaagtg 660  
 ctttttaatt aaatgaagcc aagtgggatt tgcataaagt gaatgtttac catgaagata 720  
 aactgttctt gactttatac tattttgaat tc 752

<210> 19  
 <211> 269  
 <212> PRT  
 <213> Homo sapiens

<400> 19

Met Gly Ala Arg Gly Ala Pro Ser Arg Arg Arg Gln Ala Gly Arg Arg  
 1 5 10 15

Leu Arg Tyr Leu Pro Thr Gly Ser Phe Pro Phe Leu Leu Leu Leu Leu  
 20 25 30

Leu Leu Cys Ile Gln Leu Gly Gly Gly Gln Lys Lys Lys Glu Asn Leu  
 35 40 45



Leu Ala Glu Lys Val Glu Gln Leu Met Glu Trp Ser Ser Arg Arg Ser  
50 55 60

Ile Phe Arg Met Asn Gly Asp Lys Phe Arg Lys Phe Ile Lys Ala Pro  
65 70 75 80

Pro Arg Asn Tyr Ser Met Ile Val Met Phe Thr Ala Leu Gln Pro Gln  
85 90 95

Arg Gln Cys Ser Val Cys Arg Gln Ala Asn Glu Glu Tyr Gln Ile Leu  
100 105 110

Ala Asn Ser Trp Arg Tyr Ser Ser Ala Phe Cys Asn Lys Leu Phe Phe  
115 120 125

Ser Met Val Asp Tyr Asp Glu Gly Thr Asp Val Phe Gln Gln Leu Asn  
130 135 140

Met Asn Ser Ala Pro Thr Phe Met His Phe Pro Pro Lys Gly Arg Pro  
145 150 155 160

Lys Arg Ala Asp Thr Phe Asp Leu Gln Arg Ile Gly Phe Ala Ala Glu  
165 170 175

Gln Leu Ala Lys Trp Ile Ala Asp Arg Thr Asp Val His Ile Arg Val  
180 185 190

Phe Arg Pro Pro Asn Tyr Ser Gly Thr Ile Ala Leu Ala Leu Leu Val  
195 200 205

Ser Leu Val Gly Gly Leu Leu Tyr Leu Arg Arg Asn Asn Leu Glu Phe  
210 215 220

Ile Tyr Asn Lys Thr Gly Trp Ala Met Val Ser Leu Cys Ile Val Phe  
225 230 235 240

Ala Met Thr Ser Gly Gln Met Trp Asn His Ile Arg Gly Pro Pro Tyr  
245 250 255

Ala His Lys Asn Pro His Asn Gly Gln Val Leu Phe Asn  
260 265

<210> 20  
<211> 891  
<212> DNA  
<213> Homo sapiens

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attgttatgt tctactgctct tcagcctcag cggcagtgtt ctgtgtgcag gcaagctaata 180  
gaagaatatc aaatactggc gaactcctgg cgctattcat ctgctttttg taacaagctc 240  
ttcttcagta tgggtggacta tgatgagggg acagacgttt ttcagcagct caacatgaac 300  
tctgctccta cattcatgca ttttcctcca aaaggcagac ctaagagagc tgatactttt 360  
gacctccaaa gaattgggatt tgcagctgag caactagcaa agtggattgc tgacagaacg 420  
gatgttcata ttcgggtttt cagaccaccc aactactctg gtaccattgc tttggccctg 480  
ttagtgctgc ttgttggagg tttgctttat ttgagaagga acaacttgga gttcatctat 540  
aacaagactg gttgggcat ggtgtctctg tgtatagtct ttgctatgac ttctggccag 600  
atgtggaacc atatccgtgg acctccatat gtcataaga acccacacaa tggacaagtg 660  
agctacattc atgggagcag ccaggctcag tttgtggcag aatcacacat tattctggta 720  
ctgaatgccg ctatcaccat ggggatggtt cttctaaatg aagcagcaac ttcgaaaggc 780  
gatgttgga aaagacggac tttttaatta aatgaagcca agtgggattt gcataaagtg 840  
aatgtttacc atgaagataa actgttctctg actttatact attttgaatt c 891

<210> 21  
<211> 314  
<212> PRT  
<213> Homo sapiens

<400> 21  
Met Gly Ala Arg Gly Ala Pro Ser Arg Arg Arg Gln Ala Gly Arg Arg  
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Leu Arg Tyr Leu Pro Thr Gly Ser Phe Pro Phe Leu Leu Leu Leu Leu  
20 25 30  
Leu Leu Cys Ile Gln Leu Gly Gly Gly Gln Lys Lys Lys Glu Asn Leu  
35 40 45  
Leu Ala Glu Lys Val Glu Gln Leu Met Glu Trp Ser Ser Arg Arg Ser  
50 55 60  
Ile Phe Arg Met Asn Gly Asp Lys Phe Arg Lys Phe Ile Lys Ala Pro  
65 70 75 80  
Pro Arg Asn Tyr Ser Met Ile Val Met Phe Thr Ala Leu Gln Pro Gln

				85						90						95
Arg	Gln	Cys	Ser	Val	Cys	Arg	Gln	Ala	Asn	Glu	Glu	Tyr	Gln	Ile	Leu	
			100					105					110			
Ala	Asn	Ser	Trp	Arg	Tyr	Ser	Ser	Ala	Phe	Cys	Asn	Lys	Leu	Phe	Phe	
		115					120					125				
Ser	Met	Val	Asp	Tyr	Asp	Glu	Gly	Thr	Asp	Val	Phe	Gln	Gln	Leu	Asn	
	130					135					140					
Met	Asn	Ser	Ala	Pro	Thr	Phe	Met	His	Phe	Pro	Pro	Lys	Gly	Arg	Pro	
145					150					155					160	
Lys	Arg	Ala	Asp	Thr	Phe	Asp	Leu	Gln	Arg	Ile	Gly	Phe	Ala	Ala	Glu	
				165					170					175		
Gln	Leu	Ala	Lys	Trp	Ile	Ala	Asp	Arg	Thr	Asp	Val	His	Ile	Arg	Val	
			180				185						190			
Phe	Arg	Pro	Pro	Asn	Tyr	Ser	Gly	Thr	Ile	Ala	Leu	Ala	Leu	Leu	Val	
		195					200					205				
Ser	Leu	Val	Gly	Gly	Leu	Leu	Tyr	Leu	Arg	Arg	Asn	Asn	Leu	Glu	Phe	
	210					215					220					
Ile	Tyr	Asn	Lys	Thr	Gly	Trp	Ala	Met	Val	Ser	Leu	Cys	Ile	Val	Phe	
225					230					235					240	
Ala	Met	Thr	Ser	Gly	Gln	Met	Trp	Asn	His	Ile	Arg	Gly	Pro	Pro	Tyr	
				245					250					255		
Ala	His	Lys	Asn	Pro	His	Asn	Gly	Gln	Val	Ser	Tyr	Ile	His	Gly	Ser	
			260					265					270			
Ser	Gln	Ala	Gln	Phe	Val	Ala	Glu	Ser	His	Ile	Ile	Leu	Val	Leu	Asn	
	275						280					285				
Ala	Ala	Ile	Thr	Met	Gly	Met	Val	Leu	Leu	Asn	Glu	Ala	Ala	Thr	Ser	
	290					295					300					
Lys	Gly	Asp	Val	Gly	Lys	Arg	Arg	Thr	Phe							
305					310											

<210> 22  
 <211> 1010

<212> DNA  
 <213> Homo sapiens

<400> 22  
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 attgttatgt tcaactgctct tcagcctcag cggcagtgtt ctgtgtgcag gcaagctaata 180  
 gaagaatatc aaatactggc gaactcctgg cgctattcat ctgctttttg taacaagctc 240  
 ttcttcagta tgggtggacta tgatgagggg acagacgttt ttcagcagct caacatgaac 300  
 tctgctccta cattcatgca ttttcctcca aaaggcagac ctaagagagc tgatactttt 360  
 gacctccaaa gaattggatt tgcagctgag caactagcaa agtggattgc tgacagaacg 420  
 gatgttcata ttcgggtttt cagaccaccc aactactctg gtaccattgc tttggccctg 480  
 ttagtgctgc ttgttggagg tttgctttat ttgagaagga acaacttggg gttcatctat 540  
 aacaagactg gttggggccat ggtgtctctg tgtatagtct ttgctatgac ttctggccag 600  
 atgtggaacc atatccgtgg acctccatat gtcataaga acccacacaa tggacaagtg 660  
 ttttaaccatt ctggaacatt gtgttcagag ccagaaaaat taatagattt tattcacatc 720  
 tatgtctacg gcttccttga caactactgc agatgccgct atcaccatgg ggatggttct 780  
 tctaaatgaa gcagcaactt cgaaaggcga tgttggaaaa agacggataa tttgcctagt 840  
 gggattgggc ctggtggtct tcttcttcag ttttctactt tcaatatattc gttccaagta 900  
 ccacggctat ccttatagct ttttaattaa atgaagccaa gtgggatttg cataaagtga 960  
 atgtttacca tgaagataaa ctgttcctga ctttatacta ttttgaattc 1010

<210> 23  
 <211> 308  
 <212> PRT  
 <213> Homo sapiens

<400> 23  
 Met Gly Ala Arg Gly Ala Pro Ser Arg Arg Arg Gln Ala Gly Arg Arg  
 1 5 10 15  
 Leu Arg Tyr Leu Pro Thr Gly Ser Phe Pro Phe Leu Leu Leu Leu Leu  
 20 25 30  
 Leu Leu Cys Ile Gln Leu Gly Gly Gly Gln Lys Lys Lys Glu Asn Leu  
 35 40 45  
 Leu Ala Glu Lys Val Glu Gln Leu Met Glu Trp Ser Ser Arg Arg Ser  
 50 55 60

Ile Phe Arg Met Asn Gly Asp Lys Phe Arg Lys Phe Ile Lys Ala Pro  
 65 70 75 80

Pro Arg Asn Tyr Ser Met Ile Val Met Phe Thr Ala Leu Gln Pro Gln  
 85 90 95

Arg Gln Cys Ser Val Cys Arg Gln Ala Asn Glu Glu Tyr Gln Ile Leu  
 100 105 110

Ala Asn Ser Trp Arg Tyr Ser Ser Ala Phe Cys Asn Lys Leu Phe Phe  
 115 120 125

Ser Met Val Asp Tyr Asp Glu Gly Thr Asp Val Phe Gln Gln Leu Asn  
 130 135 140

Met Asn Ser Ala Pro Thr Phe Met His Phe Pro Pro Lys Gly Arg Pro  
 145 150 155 160

Lys Arg Ala Asp Thr Phe Asp Leu Gln Arg Ile Gly Phe Ala Ala Glu  
 165 170 175

Gln Leu Ala Lys Trp Ile Ala Asp Arg Thr Asp Val His Ile Arg Val  
 180 185 190

Phe Arg Pro Pro Asn Tyr Ser Gly Thr Ile Ala Leu Ala Leu Leu Val  
 195 200 205

Ser Leu Val Gly Gly Leu Leu Tyr Leu Arg Arg Asn Asn Leu Glu Phe  
 210 215 220

Ile Tyr Asn Lys Thr Gly Trp Ala Met Val Ser Leu Cys Ile Val Phe  
 225 230 235 240

Ala Met Thr Ser Gly Gln Met Trp Asn His Ile Arg Gly Pro Pro Tyr  
 245 250 255

Ala His Lys Asn Pro His Asn Gly Gln Val Phe Asn His Ser Gly Thr  
 260 265 270

Leu Cys Ser Glu Pro Glu Lys Leu Ile Asp Phe Ile His Ile Tyr Val  
 275 280 285

Tyr Gly Phe Leu Asp Asn Tyr Cys Arg Cys Arg Tyr His His Gly Asp  
 290 295 300

Gly Ser Ser Lys  
305

<210> 24  
<211> 919  
<212> DNA  
<213> Homo sapiens

<400> 24  
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attgttatgt tcaactgctct tcagcctcag cggcagtggt ctgtgtgcag gcaagctaata 180  
gaagaatatc aaataactggc gaactcctgg cgctattcat ctgctttttg taacaagctc 240  
ttcttcagta tgggtggacta tgatgagggg acagacgttt ttcagcagct caacatgaac 300  
tctgctccta cattcatgca ttttcctcca aaaggcagac ctaagagagc tgatactttt 360  
gacctccaaa gaattgggatt tgcagctgag caactagcaa agtggattgc tgacagaacg 420  
gatgttcata ttcgggtttt cagaccaccc aactactctg gtaccattgc tttggccctg 480  
ttagtgctgc ttggtggagg tttgctttat ttgagaagga acaacttgga gttcatctat 540  
aacaagactg gttgggccat ggtgtctctg tgtatagtct ttgctatgac ttctggccag 600  
atgtggaacc atatccgtgg acctccatat gctcataaga acccacacaa tggacaagtg 660  
tttaaccatt ctggaacatt gtgttcagag ccagaaaaat taatagattt tattcacatc 720  
tatgtctacg gcttccttga caactactgc agatgccgct atcaccatgg ggatgggttct 780  
tctaaatgaa gcagcaactt cgaaaggcga tggttgaaaa agacggactt tttaattaaa 840  
tgaagccaag tgggatttgc ataaagtga tgtttaccat gaagataaac tgttcctgac 900  
tttatactat tttgaattc 919

<210> 25  
<211> 308  
<212> PRT  
<213> Homo sapiens

<400> 25

Met Gly Ala Arg Gly Ala Pro Ser Arg Arg Arg Gln Ala Gly Arg Arg  
1 5 10 15

Leu Arg Tyr Leu Pro Thr Gly Ser Phe Pro Phe Leu Leu Leu Leu Leu  
20 25 30

Leu Leu Cys Ile Gln Leu Gly Gly Gly Gln Lys Lys Lys Glu Asn Leu  
35 40 45

Leu Ala Glu Lys Val Glu Gln Leu Met Glu Trp Ser Ser Arg Arg Ser  
 50 55 60

Ile Phe Arg Met Asn Gly Asp Lys Phe Arg Lys Phe Ile Lys Ala Pro  
 65 70 75 80

Pro Arg Asn Tyr Ser Met Ile Val Met Phe Thr Ala Leu Gln Pro Gln  
 85 90 95

Arg Gln Cys Ser Val Cys Arg Gln Ala Asn Glu Glu Tyr Gln Ile Leu  
 100 105 110

Ala Asn Ser Trp Arg Tyr Ser Ser Ala Phe Cys Asn Lys Leu Phe Phe  
 115 120 125

Ser Met Val Asp Tyr Asp Glu Gly Thr Asp Val Phe Gln Gln Leu Asn  
 130 135 140

Met Asn Ser Ala Pro Thr Phe Met His Phe Pro Pro Lys Gly Arg Pro  
 145 150 155 160

Lys Arg Ala Asp Thr Phe Asp Leu Gln Arg Ile Gly Phe Ala Ala Glu  
 165 170 175

Gln Leu Ala Lys Trp Ile Ala Asp Arg Thr Asp Val His Ile Arg Val  
 180 185 190

Phe Arg Pro Pro Asn Tyr Ser Gly Thr Ile Ala Leu Ala Leu Leu Val  
 195 200 205

Ser Leu Val Gly Gly Leu Leu Tyr Leu Arg Arg Asn Asn Leu Glu Phe  
 210 215 220

Ile Tyr Asn Lys Thr Gly Trp Ala Met Val Ser Leu Cys Ile Val Phe  
 225 230 235 240

Ala Met Thr Ser Gly Gln Met Trp Asn His Ile Arg Gly Pro Pro Tyr  
 245 250 255

Ala His Lys Asn Pro His Asn Gly Gln Val Phe Asn His Ser Gly Thr  
 260 265 270

Leu Cys Ser Glu Pro Glu Lys Leu Ile Asp Phe Ile His Ile Tyr Val  
 275 280 285

Tyr Gly Phe Leu Asp Asn Tyr Cys Arg Cys Arg Tyr His His Gly Asp  
 290 295 300

Gly Ser Ser Lys  
 305

<210> 26  
 <211> 335  
 <212> PRT  
 <213> Homo sapiens

<400> 26

Met Ala Ala Arg Trp Arg Phe Trp Cys Val Ser Val Thr Met Val Val  
 1 5 10 15

Ala Leu Leu Ile Val Cys Asp Val Pro Ser Ala Ser Ala Gln Arg Lys  
 20 25 30

Lys Glu Met Val Leu Ser Glu Lys Val Ser Gln Leu Met Glu Trp Thr  
 35 40 45

Asn Lys Arg Pro Val Ile Arg Met Asn Gly Asp Lys Phe Arg Arg Leu  
 50 55 60

Val Lys Ala Pro Pro Arg Asn Tyr Ser Val Ile Val Met Phe Thr Ala  
 65 70 75 80

Leu Gln Leu His Arg Gln Cys Val Val Cys Lys Gln Ala Asp Glu Glu  
 85 90 95

Phe Gln Ile Leu Ala Asn Ser Trp Arg Tyr Ser Ser Ala Phe Thr Asn  
 100 105 110

Arg Ile Phe Phe Ala Met Val Asp Phe Asp Glu Gly Ser Asp Val Phe  
 115 120 125

Gln Met Leu Asn Met Asn Ser Ala Pro Thr Phe Ile Asn Phe Pro Ala  
 130 135 140

Lys Gly Lys Pro Lys Arg Gly Asp Thr Tyr Glu Leu Gln Val Arg Gly  
 145 150 155 160

Phe Ser Ala Glu Gln Ile Ala Arg Trp Ile Ala Asp Arg Thr Asp Val  
 165 170 175

Asn Ile Arg Val Ile Arg Pro Pro Asn Tyr Ala Gly Pro Leu Met Leu  
 180 185 190



Gly Leu Leu Leu Ala Val Ile Gly Gly Leu Val Tyr Leu Arg Arg Ser  
 195 200 205

Asn Met Glu Phe Leu Phe Asn Lys Thr Gly Trp Ala Phe Ala Ala Leu  
 210 215 220

Cys Phe Val Leu Ala Met Thr Ser Gly Gln Met Trp Asn His Ile Arg  
 225 230 235 240

Gly Pro Pro Tyr Ala His Lys Asn Pro His Thr Gly His Val Asn Tyr  
 245 250 255

Ile His Gly Ser Ser Gln Ala Gln Phe Val Ala Glu Thr His Ile Val  
 260 265 270

Leu Leu Phe Asn Gly Gly Val Thr Leu Gly Met Val Leu Leu Cys Glu  
 275 280 285

Ala Ala Thr Ser Asp Met Asp Ile Gly Lys Arg Lys Ile Met Cys Val  
 290 295 300

Ala Gly Ile Gly Leu Val Val Leu Phe Phe Ser Trp Met Leu Ser Ile  
 305 310 315 320

Phe Arg Ser Lys Tyr His Gly Tyr Pro Tyr Ser Phe Leu Met Ser  
 325 330 335

<210> 27  
 <211> 348  
 <212> PRT  
 <213> Homo sapiens

<400> 27

Met Gly Ala Arg Gly Ala Pro Ser Arg Arg Arg Gln Ala Gly Arg Arg  
 1 5 10 15

Leu Arg Tyr Leu Pro Thr Gly Ser Phe Pro Phe Leu Leu Leu Leu Leu  
 20 25 30

Leu Leu Cys Ile Gln Leu Gly Gly Gly Gln Lys Lys Lys Glu Asn Leu  
 35 40 45

Leu Ala Glu Lys Val Glu Gln Leu Met Glu Trp Ser Ser Arg Arg Ser  
 50 55 60

Ile Phe Arg Met Asn Gly Asp Lys Phe Arg Lys Phe Ile Lys Ala Pro  
 65 70 75 80  
 Pro Arg Asn Tyr Ser Met Ile Val Met Phe Thr Ala Leu Gln Pro Gln  
 85 90 95  
 Arg Gln Cys Ser Val Cys Arg Gln Ala Asn Glu Glu Tyr Gln Ile Leu  
 100 105 110  
 Ala Asn Ser Trp Arg Tyr Ser Ser Ala Phe Cys Asn Lys Leu Phe Phe  
 115 120 125  
 Ser Met Val Asp Tyr Asp Glu Gly Thr Asp Val Phe Gln Gln Leu Asn  
 130 135 140  
 Met Asn Ser Ala Pro Thr Phe Met His Phe Pro Pro Lys Gly Arg Pro  
 145 150 155 160  
 Lys Arg Ala Asp Thr Phe Asp Leu Gln Arg Ile Gly Phe Ala Ala Glu  
 165 170 175  
 Gln Leu Ala Lys Trp Ile Ala Asp Arg Thr Asp Val His Ile Arg Val  
 180 185 190  
 Phe Arg Pro Pro Asn Tyr Ser Gly Thr Ile Ala Leu Ala Leu Leu Val  
 195 200 205  
 Ser Leu Val Gly Gly Leu Leu Tyr Leu Arg Arg Asn Asn Leu Glu Phe  
 210 215 220  
 Ile Tyr Asn Lys Thr Gly Trp Ala Met Val Ser Leu Cys Ile Val Phe  
 225 230 235 240  
 Ala Met Thr Ser Gly Gln Met Trp Asn His Ile Arg Gly Pro Pro Tyr  
 245 250 255  
 Ala His Lys Asn Pro His Asn Gly Gln Val Ser Tyr Ile His Gly Ser  
 260 265 270  
 Ser Gln Ala Gln Phe Val Ala Glu Ser His Ile Ile Leu Val Leu Asn  
 275 280 285  
 Ala Ala Ile Thr Met Gly Met Val Leu Leu Asn Glu Ala Ala Thr Ser  
 290 295 300  
 Lys Gly Asp Val Gly Lys Arg Arg Ile Ile Cys Leu Val Gly Leu Gly



Gln Leu Ala Lys Trp Ile Ala Asp Arg Thr Asp Val His Ile Arg Val  
180 185 190

Phe Arg Pro Pro Asn Tyr Ser Gly Thr Ile Ala Leu Ala Leu Leu Val  
195 200 205

Ser Leu Val Gly Gly Leu Leu Tyr Leu Arg Arg Asn Asn Leu Glu Phe  
210 215 220

Ile Tyr Asn Lys Thr Gly Trp Ala Met Val Ser Leu Cys Ile Val Phe  
225 230 235 240

Ala Met Thr Ser Gly Gln Met Trp Asn His Ile Arg Gly Pro Pro Tyr  
245 250 255

Ala His Lys Asn Pro His Asn Gly Gln Val Ser Tyr Ile His Gly Ser  
260 265 270

Ser Gln Ala Gln Phe Val Ala Glu Ser His Ile Ile Leu Val Leu Asn  
275 280 285

Ala Ala Ile Thr Met Gly Met Val Leu Leu Asn Glu Ala Ala Thr Ser  
290 295 300

Lys Gly Asp Val Gly Lys Arg Arg Ile Ile Cys Leu Val Gly Leu Gly  
305 310 315 320

Leu Val Val Phe Phe Phe Ser Phe Leu Leu Ser Ile Phe Arg Ser Lys  
325 330 335

Tyr His Gly Tyr Pro Tyr Ser Phe Leu Ile Lys  
340 345

<210> 29  
<211> 350  
<212> PRT  
<213> Homo sapiens

<400> 29

Met Gly Ala Arg Gly Ala Pro Ser Arg Arg Arg Gln Ala Gly Arg Arg  
1 5 10 15

Leu Arg Tyr Leu Pro Thr Gly Ser Phe Pro Phe Leu Leu Leu Leu Leu  
20 25 30

Leu Leu Cys Ile Gln Leu Gly Gly Gly Gln Lys Lys Lys Glu Asn Leu

35	40	45																	
Leu	Ala	Glu	Lys	Val	Glu	Gln	Leu	Met	Glu	Trp	Ser	Ser	Arg	Arg	Ser				
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Ile	Phe	Arg	Met	Asn	Gly	Asp	Lys	Phe	Arg	Lys	Phe	Ile	Lys	Ala	Pro				
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Pro	Arg	Asn	Tyr	Ser	Met	Ile	Val	Met	Phe	Thr	Ala	Leu	Gln	Pro	Gln				
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Arg	Gln	Cys	Ser	Val	Cys	Arg	Gln	Ala	Asn	Glu	Glu	Tyr	Gln	Ile	Leu				
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Ala	Asn	Ser	Trp	Arg	Tyr	Ser	Ser	Ala	Phe	Cys	Asn	Lys	Leu	Phe	Phe				
		115					120					125							
Ser	Met	Val	Asp	Tyr	Asp	Glu	Gly	Thr	Asp	Val	Phe	Gln	Gln	Leu	Asn				
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Met	Asn	Ser	Ala	Pro	Thr	Phe	Met	His	Phe	Pro	Pro	Lys	Gly	Arg	Pro				
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Lys	Arg	Ala	Asp	Thr	Phe	Asp	Leu	Gln	Arg	Ile	Gly	Phe	Ala	Ala	Glu				
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Gln	Leu	Ala	Lys	Trp	Ile	Ala	Asp	Arg	Thr	Asp	Val	His	Ile	Arg	Val				
			180					185					190						
Phe	Arg	Pro	Pro	Asn	Tyr	Ser	Gly	Thr	Ile	Ala	Leu	Ala	Leu	Leu	Val				
		195					200					205							
Ser	Leu	Val	Gly	Gly	Leu	Leu	Tyr	Leu	Arg	Arg	Asn	Asn	Leu	Glu	Phe				
	210					215					220								
Ile	Tyr	Asn	Lys	Thr	Gly	Trp	Ala	Met	Val	Ser	Leu	Cys	Ile	Val	Phe				
225					230					235				240					
Ala	Met	Thr	Ser	Gly	Gln	Met	Trp	Asn	His	Ile	Arg	Gly	Pro	Pro	Tyr				
				245					250				255						
Ala	His	Lys	Asn	Pro	His	Asn	Gly	Gln	Val	Ser	Tyr	Ile	His	Gly	Ser				
			260					265					270						
Ser	Gln	Ala	Gln	Phe	Val	Ala	Glu	Ser	His	Ile	Ile	Leu	Val	Leu	Asn				
	275						280					285							

Ala Ala Ile Thr Met Gly Met Val Leu Leu Asn Glu Ala Ala Thr Ser  
 290 295 300

Lys Gly Asp Val Gly Lys Arg Arg Thr Phe Ile Ile Cys Leu Val Gly  
 305 310 315 320

Leu Gly Leu Val Val Phe Phe Phe Ser Phe Leu Leu Ser Ile Phe Arg  
 325 330 335

Ser Lys Tyr His Gly Tyr Pro Tyr Ser Asp Leu Asp Phe Glu  
 340 345 350

<210> 30  
 <211> 347  
 <212> PRT  
 <213> Drosophila melanogaster

<400> 30

Met Arg Leu Leu His Lys Thr Leu Leu Ser Gly Leu Leu Val Val Ala  
 1 5 10 15

Leu Phe Ala Ile Tyr Ala Ala Ala Gln Ser Lys Ser Lys Thr Gly Leu  
 20 25 30

Ser Leu Ser Glu Lys Val Gln Asn Leu Val Asp Met Asn Ala Lys Lys  
 35 40 45

Pro Leu Leu Arg Phe Asn Gly Pro Lys Phe Arg Glu Tyr Val Lys Ser  
 50 55 60

Ala Pro Arg Asn Tyr Ser Met Ile Val Met Leu Thr Ala Leu Ala Pro  
 65 70 75 80

Ser Arg Gln Cys Gln Ile Cys Arg His Ala His Asp Glu Phe Ala Ile  
 85 90 95

Val Ala Asn Ser Tyr Arg Phe Ser Ser Thr Tyr Ser Asn Lys Leu Phe  
 100 105 110

Phe Ala Met Val Asp Phe Asp Asp Gly Ser Glu Val Phe Gln Leu Leu  
 115 120 125

Arg Leu Asn Thr Ala Pro Val Phe Met His Phe Pro Ala Lys Gly Lys  
 130 135 140

Pro Lys Gly Ala Asp Thr Met Asp Ile His Arg Val Gly Phe Ala Ala  
 145 150 155 160

Asp Ser Ile Ala Lys Phe Val Ala Glu Arg Thr Asp Ile Thr Ile Arg  
 165 170 175

Ile Phe Arg Pro Pro Asn Tyr Ser Gly Thr Val Ala Met Ile Thr Leu  
 180 185 190

Val Ala Leu Val Gly Ser Phe Leu Tyr Ile Arg Arg Asn Asn Leu Glu  
 195 200 205

Phe Leu Tyr Asn Lys Asn Leu Trp Gly Ala Ile Ala Val Phe Phe Cys  
 210 215 220

Phe Ala Met Ile Ser Gly Gln Met Trp Asn His Ile Arg Gly Pro Pro  
 225 230 235 240

Leu Val His Lys Ser Gln Asn Gly Gly Val Ala Tyr Ile His Gly Ser  
 245 250 255

Ser Gln Gly Gln Leu Val Val Glu Thr Tyr Ile Val Met Phe Leu Asn  
 260 265 270

Ala Met Ile Val Leu Gly Met Ile Leu Leu Ile Glu Ser Gly Thr Pro  
 275 280 285

Lys Ala His Asn Lys Asn Arg Ile Met Ala Met Thr Gly Leu Val Leu  
 290 295 300

Leu Thr Val Phe Phe Ser Phe Leu Leu Ser Val Phe Arg Ser Lys Ala  
 305 310 315 320

Gln Gly Tyr Pro Tyr Ile Ser Cys Ser Asn Arg Ile Asp Cys Ser Pro  
 325 330 335

Val Pro Val Gln Val His Pro Ile Ser Phe Leu  
 340 345

<210> 31  
 <211> 331  
 <212> PRT  
 <213> Caenorhabditis elegans

<400> 31

Met Leu Leu Ala Val Tyr Glu Ser Ala Gln Gln Gln Thr Leu Glu Asp  
 1 5 10 15

Lys Val Gln Asn Leu Val Asp Leu Thr Ser Arg Gln Ser Ile Val Lys  
 20 25 30

Phe Asn Met Asp Lys Trp Lys Thr Leu Val Arg Met Gln Pro Arg Asn  
 35 40 45

Tyr Ser Met Ile Val Met Phe Thr Ala Leu Ser Pro Gly Val Gln Cys  
 50 55 60

Pro Ile Cys Lys Pro Ala Tyr Asp Glu Phe Met Ile Val Ala Asn Ser  
 65 70 75 80

His Arg Tyr Thr Ser Ser Glu Gly Asp Arg Arg Lys Val Phe Phe Gly  
 85 90 95

Ile Val Asp Tyr Glu Asp Ala Pro Gln Ile Phe Gln Gln Met Asn Leu  
 100 105 110

Asn Thr Ala Pro Ile Leu Tyr His Phe Gly Pro Lys Leu Gly Ala Lys  
 115 120 125

Lys Arg Pro Glu Gln Met Asp Phe Gln Arg Gln Gly Phe Asp Ala Asp  
 130 135 140

Ala Ile Gly Arg Phe Val Ala Asp Gln Thr Glu Val His Val Arg Val  
 145 150 155 160

Ile Arg Pro Pro Asn Tyr Thr Ala Pro Val Val Ile Ala Leu Phe Val  
 165 170 175

Ala Leu Leu Leu Gly Met Leu Tyr Met Lys Arg Asn Ser Leu Asp Phe  
 180 185 190

Leu Phe Asn Arg Thr Val Trp Gly Phe Val Cys Leu Ala Ile Thr Phe  
 195 200 205

Ile Phe Met Ser Gly Gln Met Trp Asn His Ile Arg Gly Pro Pro Phe  
 210 215 220

Met Ile Thr Asn Pro Asn Thr Lys Glu Pro Ser Phe Ile His Gly Ser  
 225 230 235 240

Thr Gln Phe Gln Leu Ile Ala Glu Thr Tyr Ile Val Gly Leu Leu Tyr  
 245 250 255



Ala Leu Ile Ala Ile Gly Phe Ile Cys Val Asn Glu Ala Ala Asp Gln  
260 265 270

Ser Asn Ser Lys Asp Arg Lys Asn Ala Gly Lys Lys Leu Asn Pro Leu  
275 280 285

Ser Leu Leu Asn Ile Pro Thr Asn Thr Leu Ala Ile Ala Gly Leu Val  
290 295 300

Cys Ile Cys Val Phe Phe Ser Phe Leu Leu Ser Val Phe Arg Ser Lys  
305 310 315 320

Tyr Arg Gly Tyr Pro Tyr Ser Phe Leu Phe Ala  
325 330

<210> 32  
<211> 350  
<212> PRT  
<213> *Saccharomyces cerevisiae*

<400> 32

Met Asn Trp Leu Phe Leu Val Ser Leu Val Phe Phe Cys Gly Val Ser  
1 5 10 15

Thr His Pro Ala Leu Ala Met Ser Ser Asn Arg Leu Leu Lys Leu Ala  
20 25 30

Asn Lys Ser Pro Lys Lys Ile Ile Pro Leu Lys Asp Ser Ser Phe Glu  
35 40 45

Asn Ile Leu Ala Pro Pro His Glu Asn Ala Tyr Ile Val Ala Leu Phe  
50 55 60

Thr Ala Thr Ala Pro Glu Ile Gly Cys Ser Leu Cys Leu Glu Leu Glu  
65 70 75 80

Ser Glu Tyr Asp Thr Ile Val Ala Ser Trp Phe Asp Asp His Pro Asp  
85 90 95

Ala Lys Ser Ser Asn Ser Asp Thr Ser Ile Phe Phe Thr Lys Val Asn  
100 105 110

Leu Glu Asp Pro Ser Lys Thr Ile Pro Lys Ala Phe Gln Phe Phe Gln  
115 120 125

Leu Asn Asn Val Pro Arg Leu Phe Ile Phe Lys Pro Asn Ser Pro Ser

130		135		140
Ile Leu Asp His Ser Val Ile Ser Ile Ser Thr Asp Thr Gly Ser Glu				
145		150		155
				160
Arg Met Lys Gln Ile Ile Gln Ala Ile Lys Gln Phe Ser Gln Val Asn				
		165		170
				175
Asp Phe Ser Leu His Leu Pro Met Asp Trp Thr Pro Ile Ile Thr Ser				
		180		185
				190
Thr Ile Ile Thr Phe Ile Thr Val Leu Leu Phe Lys Lys Gln Ser Lys				
		195		200
				205
Leu Met Phe Ser Ile Ile Ser Ser Arg Ile Ile Trp Ala Thr Leu Ser				
		210		215
				220
Thr Phe Phe Ile Ile Cys Met Ile Ser Ala Tyr Met Phe Asn Gln Ile				
225		230		235
				240
Arg Asn Thr Gln Leu Ala Gly Val Gly Pro Lys Gly Glu Val Met Tyr				
		245		250
				255
Phe Leu Pro Asn Glu Phe Gln His Gln Phe Ala Ile Glu Thr Gln Val				
		260		265
				270
Met Val Leu Ile Tyr Gly Thr Leu Ala Ala Leu Val Val Val Leu Val				
		275		280
				285
Lys Gly Ile Gln Phe Leu Arg Ser His Leu Tyr Pro Glu Thr Lys Lys				
		290		295
				300
Ala Tyr Phe Ile Asp Ala Ile Leu Ala Ser Phe Cys Ala Leu Phe Ile				
305		310		315
				320
Tyr Val Phe Phe Ala Ala Leu Thr Thr Val Phe Thr Ile Lys Ser Pro				
		325		330
				335
Ala Tyr Pro Phe Pro Leu Leu Arg Leu Ser Ala Pro Phe Lys				
		340		345
				350

<210> 33  
 <211> 332  
 <212> PRT  
 <213> *Saccharomyces cerevisiae*  
 <400> 33

Met	Lys	Trp	Cys	Ser	Thr	Tyr	Ile	Ile	Ile	Trp	Leu	Ala	Ile	Ile	Phe	1	5	10	15
His	Lys	Phe	Gln	Lys	Ser	Thr	Ala	Thr	Ala	Ser	His	Asn	Ile	Asp	Asp	20	25	30	
Ile	Leu	Gln	Leu	Lys	Asp	Asp	Thr	Gly	Val	Ile	Thr	Val	Thr	Ala	Asp	35	40	45	
Asn	Tyr	Pro	Leu	Leu	Ser	Arg	Gly	Val	Pro	Gly	Tyr	Phe	Asn	Ile	Leu	50	55	60	
Tyr	Ile	Thr	Met	Arg	Gly	Thr	Asn	Ser	Asn	Gly	Met	Ser	Cys	Gln	Leu	65	70	75	80
Cys	His	Asp	Phe	Glu	Lys	Thr	Tyr	His	Ala	Val	Ala	Asp	Val	Ile	Arg	85	90	95	
Ser	Gln	Ala	Pro	Gln	Ser	Leu	Asn	Leu	Phe	Phe	Thr	Val	Asp	Val	Asn	100	105	110	
Glu	Val	Pro	Gln	Leu	Val	Lys	Asp	Leu	Lys	Leu	Gln	Asn	Val	Pro	His	115	120	125	
Leu	Val	Val	Tyr	Pro	Pro	Ala	Glu	Ser	Asn	Lys	Gln	Ser	Gln	Phe	Glu	130	135	140	
Trp	Lys	Thr	Ser	Pro	Phe	Tyr	Gln	Tyr	Ser	Leu	Val	Pro	Glu	Asn	Ala	145	150	155	160
Glu	Asn	Thr	Leu	Gln	Phe	Gly	Asp	Phe	Leu	Ala	Lys	Ile	Leu	Asn	Ile	165	170	175	
Ser	Ile	Thr	Val	Pro	Gln	Ala	Phe	Asn	Val	Gln	Glu	Phe	Val	Tyr	Tyr	180	185	190	
Phe	Val	Ala	Cys	Met	Val	Val	Phe	Ile	Phe	Ile	Lys	Lys	Val	Ile	Leu	195	200	205	
Pro	Lys	Val	Thr	Asn	Lys	Trp	Lys	Leu	Phe	Ser	Met	Ile	Leu	Ser	Leu	210	215	220	
Gly	Ile	Leu	Leu	Pro	Ser	Ile	Thr	Gly	Tyr	Lys	Phe	Val	Glu	Met	Asn	225	230	235	240

Ala Ile Pro Phe Ile Ala Arg Asp Ala Lys Asn Arg Ile Met Tyr Phe  
 245 250 255

Ser Gly Gly Ser Gly Trp Gln Phe Gly Ile Glu Ile Phe Ser Val Ser  
 260 265 270

Leu Met Tyr Ile Val Met Ser Ala Leu Ser Val Leu Leu Ile Tyr Val  
 275 280 285

Pro Lys Ile Ser Cys Val Ser Glu Lys Met Arg Gly Leu Leu Ser Ser  
 290 295 300

Phe Leu Ala Cys Val Leu Phe Tyr Phe Phe Ser Tyr Phe Ile Ser Cys  
 305 310 315 320

Tyr Leu Ile Lys Asn Pro Gly Tyr Pro Ile Val Phe  
 325 330

<210> 34  
 <211> 108  
 <212> PRT  
 <213> Homo sapiens

<400> 34

Leu Val Ser Leu Val Gly Gly Leu Leu Tyr Leu Arg Arg Asn Asn Leu  
 1 5 10 15

Glu Phe Ile Tyr Asn Lys Thr Gly Trp Ala Met Val Ser Leu Cys Ile  
 20 25 30

Val Phe Ala Met Thr Ser Gly Gln Met Trp Asn His Ile Arg Gly Pro  
 35 40 45

Pro Tyr Ala His Lys Asn Pro His Asn Gly Gln Val Ser Tyr Ile His  
 50 55 60

Gly Ser Ser Gln Ala Gln Phe Val Ala Glu Ser His Ile Ile Leu Val  
 65 70 75 80

Leu Asn Ala Ala Ile Thr Met Gly Met Val Leu Leu Asn Glu Ala Ala  
 85 90 95

Thr Ser Lys Gly Asp Val Gly Lys Arg Arg Thr Phe  
 100 105

<210> 35  
 <211> 142

<212> PRT  
<213> Homo sapiens

<400> 35

Leu Val Ser Leu Val Gly Gly Leu Leu Tyr Leu Arg Arg Asn Asn Leu  
1 5 10 15

Glu Phe Ile Tyr Asn Lys Thr Gly Trp Ala Met Val Ser Leu Cys Ile  
20 25 30

Val Phe Ala Met Thr Ser Gly Gln Met Trp Asn His Ile Arg Gly Pro  
35 40 45

Pro Tyr Ala His Lys Asn Pro His Asn Gly Gln Val Ser Tyr Ile His  
50 55 60

Gly Ser Ser Gln Ala Gln Phe Val Ala Glu Ser His Ile Ile Leu Val  
65 70 75 80

Leu Asn Ala Ala Ile Thr Met Gly Met Val Leu Leu Asn Glu Ala Ala  
85 90 95

Thr Ser Lys Gly Asp Val Gly Lys Arg Arg Ile Ile Cys Leu Val Gly  
100 105 110

Leu Gly Leu Val Val Phe Phe Phe Ser Phe Leu Leu Ser Ile Phe Arg  
115 120 125

Ser Lys Tyr His Gly Tyr Pro Tyr Ser Asp Leu Asp Phe Glu  
130 135 140

<210> 36  
<211> 141  
<212> PRT  
<213> Homo sapiens

<400> 36

Leu Val Ser Leu Val Gly Gly Leu Leu Tyr Leu Arg Arg Asn Asn Leu  
1 5 10 15

Glu Phe Ile Tyr Asn Lys Thr Gly Trp Ala Met Val Ser Leu Cys Ile  
20 25 30

Val Phe Ala Met Thr Ser Gly Gln Met Trp Asn His Ile Arg Gly Pro  
35 40 45

Pro Tyr Ala His Lys Asn Pro His Asn Gly Gln Val Ser Tyr Ile His

50					55					60					
Gly	Ser	Ser	Gln	Ala	Gln	Phe	Val	Ala	Glu	Ser	His	Ile	Ile	Leu	Val
65					70					75					80
Leu	Asn	Ala	Ala	Ile	Thr	Met	Gly	Met	Val	Leu	Leu	Asn	Glu	Ala	Ala
				85					90					95	
Thr	Ser	Lys	Gly	Asp	Val	Gly	Lys	Arg	Arg	Ile	Ile	Cys	Leu	Val	Gly
			100					105					110		
Leu	Gly	Leu	Val	Val	Phe	Phe	Phe	Ser	Phe	Leu	Leu	Ser	Ile	Phe	Arg
		115					120					125			
Ser	Lys	Tyr	His	Gly	Tyr	Pro	Tyr	Ser	Phe	Leu	Ile	Lys			
	130					135					140				

Leu	Val	Ser	Leu	Val	Gly	Gly	Leu	Leu	Tyr	Leu	Arg	Arg	Asn	Asn	Leu
1				5					10					15	
Glu	Phe	Ile	Tyr	Asn	Lys	Thr	Gly	Trp	Ala	Met	Val	Ser	Leu	Cys	Ile
			20					25					30		
Val	Phe	Ala	Met	Thr	Ser	Gly	Gln	Met	Trp	Asn	His	Ile	Arg	Gly	Pro
		35					40					45			
Pro	Tyr	Ala	His	Lys	Asn	Pro	His	Asn	Gly	Gln	Val	Leu	Phe	Asn	
	50					55				60					

Leu Val Ser Leu Val Gly Gly Leu Leu Tyr Leu Arg Arg Asn Asn Leu  
1 5 10 15

Glu Phe Ile Tyr Asn Lys Thr Gly Trp Ala Met Val Ser Leu Cys Ile  
20 25 30

Val Phe Ala Met Thr Ser Gly Gln Met Trp Asn His Ile Arg Gly Pro  
 35 40 45

Pro Tyr Ala His Lys Asn Pro His Asn Gly Gln Val Phe Asn His Ser  
 50 55 60

Gly Thr Leu Cys Ser Glu Pro Glu Lys Leu Ile Asp Phe Ile His Ile  
 65 70 75 80

Tyr Val Tyr Gly Phe Leu Asp Asn Tyr Cys Arg Cys Arg Tyr His His  
 85 90 95

Gly Asp Gly Ser Ser Lys  
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<210> 39  
 <211> 102  
 <212> PRT  
 <213> Homo sapiens

<400> 39

Leu Val Ser Leu Val Gly Gly Leu Leu Tyr Leu Arg Arg Asn Asn Leu  
 1 5 10 15

Glu Phe Ile Tyr Asn Lys Thr Gly Trp Ala Met Val Ser Leu Cys Ile  
 20 25 30

Val Phe Ala Met Thr Ser Gly Gln Met Trp Asn His Ile Arg Gly Pro  
 35 40 45

Pro Tyr Ala His Lys Asn Pro His Asn Gly Gln Val Phe Asn His Ser  
 50 55 60

Gly Thr Leu Cys Ser Glu Pro Glu Lys Leu Ile Asp Phe Ile His Ile  
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Tyr Val Tyr Gly Phe Leu Asp Asn Tyr Cys Arg Cys Arg Tyr His His  
 85 90 95

Gly Asp Gly Ser Ser Lys  
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<210> 40  
 <211> 2871  
 <212> DNA  
 <213> Homo sapiens

<400> 40

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<400> 41

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 35 40 45

Lys Asn Arg Ile Asn Arg Ala Pro Glu Arg Leu Gly Lys Ala Lys Val  
 50 55 60

Glu Val Asp Ile Phe Glu Leu Leu Arg Asp Ser Glu Tyr Glu Thr Ala  
 65 70 75 80

Glu Thr Met Cys Gln Ile Leu Pro Lys Gly Val Val Ala Val Leu Gly  
 85 90 95

Pro Ser Ser Ser Pro Ala Ser Ser Ser Ile Ile Ser Asn Ile Cys Gly  
 100 105 110

Glu Lys Glu Val Pro His Phe Lys Val Ala Pro Glu Glu Phe Val Lys  
 115 120 125

Phe Gln Phe Gln Arg Phe Thr Thr Leu Asn Leu His Pro Ser Asn Thr  
 130 135 140

Asp Ile Ser Val Ala Val Ala Gly Ile Leu Asn Phe Phe Asn Cys Thr  
 145 150 155 160

Thr Ala Cys Leu Ile Cys Ala Lys Ala Glu Cys Leu Leu Asn Leu Glu  
 165 170 175

Lys Leu Leu Arg Gln Phe Leu Ile Ser Lys Asp Thr Leu Ser Val Arg  
 180 185 190

Met Leu Asp Asp Thr Arg Asp Pro Thr Pro Leu Leu Lys Glu Ile Arg  
 195 200 205

Asp Asp Lys Thr Ala Thr Ile Ile Ile His Ala Asn Ala Ser Met Ser  
 210 215 220

His Thr Ile Leu Leu Lys Ala Ala Glu Leu Gly Met Val Ser Ala Tyr  
 225 230 235 240

Tyr Thr Tyr Ile Phe Thr Asn Leu Glu Phe Ser Leu Gln Arg Thr Asp  
 245 250 255

Ser Leu Val Asp Asp Arg Val Asn Ile Leu Gly Phe Ser Ile Phe Asn  
 260 265 270

Gln Ser His Ala Phe Phe Gln Glu Phe Ala Gln Ser Leu Asn Gln Ser  
 275 280 285

Trp Gln Glu Asn Cys Asp His Val Pro Phe Thr Gly Pro Ala Leu Ser  
 290 295 300

Ser Ala Leu Leu Phe Asp Ala Val Tyr Ala Val Val Thr Ala Val Gln  
 305 310 315 320

Glu Leu Asn Arg Ser Gln Glu Ile Gly Val Lys Pro Leu Ser Cys Gly  
                             325                            330                            335

Ser Ala Gln Ile Trp Gln His Gly Thr Ser Leu Met Asn Tyr Leu Arg  
                             340                            345                            350

Met Val Glu Leu Glu Gly Leu Thr Gly His Ile Glu Phe Asn Ser Lys  
                             355                            360                            365

Gly Gln Arg Ser Asn Tyr Ala Leu Lys Ile Leu Gln Phe Thr Arg Asn  
             370                            375                            380

Gly Phe Arg Gln Ile Gly Gln Trp His Val Ala Glu Gly Leu Ser Met  
     385                            390                            395                            400

Asp Ser His Leu Tyr Ala Ser Asn Ile Ser Asp Thr Leu Phe Asn Thr  
                             405                            410                            415

Thr Leu Val Val Thr Thr Ile Leu Glu Asn Pro Tyr Leu Met Leu Lys  
                             420                            425                            430

Gly Asn His Gln Glu Met Glu Gly Asn Asp Arg Tyr Glu Gly Phe Cys  
                             435                            440                            445

Val Asp Met Leu Lys Glu Leu Ala Glu Ile Leu Arg Phe Asn Tyr Lys  
             450                            455                            460

Ile Arg Leu Val Gly Asp Gly Val Tyr Gly Val Pro Glu Ala Asn Gly  
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Thr Trp Thr Gly Met Val Gly Glu Leu Ile Ala Arg Lys Ala Asp Leu  
                             485                            490                            495

Ala Val Ala Gly Leu Thr Ile Thr Ala Glu Arg Glu Lys Val Ile Asp  
                             500                            505                            510

Phe Ser Lys Pro Phe Met Thr Leu Gly Ile Ser Ile Leu Tyr Arg Ile  
             515                            520                            525

His Met Gly Arg Lys Pro Gly Tyr Phe Ser Phe Leu Asp Pro Phe Ser  
             530                            535                            540

Pro Gly Val Trp Leu Phe Met Leu Leu Ala Tyr Leu Ala Val Ser Cys  
     545                            550                            555                            560

Val Leu Phe Leu Val Ala Arg Leu Thr Pro Tyr Glu Trp Tyr Ser Pro  
 565 570 575  
 His Pro Cys Ala Gln Gly Arg Cys Asn Leu Leu Val Asn Gln Tyr Ser  
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 Leu Gly Asn Ser Leu Trp Phe Pro Val Gly Gly Phe Met Gln Gln Gly  
 595 600 605  
 Ser Thr Ile Ala Pro Arg Ala Leu Ser Thr Arg Cys Val Ser Gly Val  
 610 615 620  
 Trp Trp Ala Phe Thr Leu Ile Ile Ile Ser Ser Tyr Thr Ala Asn Leu  
 625 630 635 640  
 Ala Ala Phe Leu Thr Val Gln Arg Met Asp Val Pro Ile Glu Ser Val  
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 Asp Asp Leu Ala Asp Gln Thr Ala Ile Glu Tyr Gly Thr Ile His Gly  
 660 665 670  
 Gly Ser Ser Met Thr Phe Phe Gln Asn Ser Arg Tyr Gln Thr Tyr Gln  
 675 680 685  
 Arg Met Trp Asn Tyr Met Tyr Ser Lys Gln Pro Ser Val Phe Val Lys  
 690 695 700  
 Ser Thr Glu Glu Gly Ile Ala Arg Val Leu Asn Ser Asn Tyr Ala Phe  
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 Leu Thr Gln Ile Gly Gly Leu Leu Asp Thr Lys Gly Tyr Gly Ile Gly  
 740 745 750  
 Met Pro Val Gly Ser Val Phe Arg Asp Glu Phe Asp Leu Ala Ile Leu  
 755 760 765  
 Gln Leu Gln Glu Asn Asn Arg Leu Glu Ile Leu Lys Arg Lys Trp Trp  
 770 775 780  
 Glu Gly Gly Lys Cys Pro Lys Glu Glu Asp His Arg Ala Lys Gly Leu  
 785 790 795 800  
 Gly Met Glu Asn Ile Gly Gly Ile Phe Val Val Leu Ile Cys Gly Leu

805	810	815	
Ile Val Ala Ile Phe Met Ala Met Leu Glu Phe Leu Trp Thr Leu Arg			
820	825	830	
His Ser Glu Ala Thr Glu Val Ser Val Cys Gln Glu Met Val Thr Glu			
835	840	845	
Leu Arg Ser Ile Ile Leu Cys Gln Asp Ser Ile His Pro Arg Arg Arg			
850	855	860	
Arg Ala Ala Val Pro Pro Pro Arg Pro Pro Ile Pro Glu Glu Arg Arg			
865	870	875	880
Pro Arg Gly Thr Ala Thr Leu Ser Asn Gly Lys Leu Cys Gly Ala Gly			
	885	890	895
Glu Pro Asp Gln Leu Ala Gln Arg Leu Ala Gln Glu Ala Ala Leu Val			
	900	905	910
Ala Arg Gly Cys Thr His Ile Arg Val Cys Pro Glu Cys Arg Arg Phe			
	915	920	925
Gln Gly Leu Arg Ala Arg Pro Ser Pro Ala Arg Ser Glu Glu Ser Leu			
	930	935	940
Glu Trp Glu Lys Thr Thr Asn Ser Ser Glu Pro Glu			
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ggtgatggga gaagcaagag agggatccac acacctgcgc ttagctttct atgacctggg			180

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<400> 44

Met Glu Ala Lys Ala  
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<210> 46  
<211> 28  
<212> PRT  
<213> Homo sapiens

<400> 46

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Met Val Ala Cys Ser Pro His Ser Leu Arg Ile Ala  
20 25

<210> 47  
<211> 193  
<212> DNA  
<213> Homo sapiens

<400> 47  
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tacgtagact ggg 193

<210> 48  
<211> 55  
<212> PRT  
<213> Homo sapiens

<400> 48

Ala Ile Leu Asp Asp Pro Met Glu Cys Ser Arg Gly Glu Arg Leu Ser  
1 5 10 15

Ile Thr Leu Ala Lys Asn Arg Ile Asn Arg Ala Pro Glu Arg Leu Gly  
20 25 30

Lys Ala Lys Val Glu Val Asp Ile Phe Glu Leu Leu Arg Asp Ser Glu  
35 40 45

Tyr Glu Thr Ala Glu Thr Met  
50 55

<210> 49

<211> 3048

<212> DNA

<213> Homo sapiens

<400> 49

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<212> PRT  
<213> Homo sapiens

<400> 50

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Gly Glu Arg Leu Ser Ile Thr Leu Ala Lys Asn Arg Ile Asn Arg Ala  
20 25 30

Pro Glu Arg Leu Gly Lys Ala Lys Val Glu Val Asp Ile Phe Glu Leu  
35 40 45

Leu Arg Asp Ser Glu Tyr Glu Thr Ala Glu Thr Met Cys Gln Ile Leu  
50 55 60

Pro Lys Gly Val Val Ala Val Leu Gly Pro Ser Ser Ser Pro Ala Ser  
65 70 75 80

Ser Ser Ile Ile Ser Asn Ile Cys Gly Glu Lys Glu Val Pro His Phe  
85 90 95

Lys Val Ala Pro Glu Glu Phe Val Lys Phe Gln Phe Gln Arg Phe Thr  
100 105 110

Thr Leu Asn Leu His Pro Ser Asn Thr Asp Ile Ser Val Ala Val Ala  
115 120 125

Gly Ile Leu Asn Phe Phe Asn Cys Thr Thr Ala Cys Leu Ile Cys Ala  
130 135 140

Lys Ala Glu Cys Leu Leu Asn Leu Glu Lys Leu Leu Arg Gln Phe Leu  
145 150 155 160

Ile Ser Lys Asp Thr Leu Ser Val Arg Met Leu Asp Asp Thr Arg Asp  
165 170 175

Pro Thr Pro Leu Leu Lys Glu Ile Arg Asp Asp Lys Thr Ala Thr Ile  
180 185 190

Ile Ile His Ala Asn Ala Ser Met Ser His Thr Ile Leu Leu Lys Ala

195	200	205
Ala Glu Leu Gly Met Val Ser	Ala Tyr Tyr Thr Tyr Ile Phe Thr Asn	
210	215	220
Leu Glu Phe Ser Leu Gln Arg Thr Asp Ser Leu Val Asp Asp Arg Val		
225	230	235 240
Asn Ile Leu Gly Phe Ser Ile Phe Asn Gln Ser His Ala Phe Phe Gln		
	245	250 255
Glu Phe Ala Gln Ser Leu Asn Gln Ser Trp Gln Glu Asn Cys Asp His		
	260	265 270
Val Pro Phe Thr Gly Pro Ala Leu Ser Ser Ala Leu Leu Phe Asp Ala		
	275	280 285
Val Tyr Ala Val Val Thr Ala Val Gln Glu Leu Asn Arg Ser Gln Glu		
	290	295 300
Ile Gly Val Lys Pro Leu Ser Cys Gly Ser Ala Gln Ile Trp Gln His		
305	310	315 320
Gly Thr Ser Leu Met Asn Tyr Leu Arg Met Val Glu Leu Glu Gly Leu		
	325	330 335
Thr Gly His Ile Glu Phe Asn Ser Lys Gly Gln Arg Ser Asn Tyr Ala		
	340	345 350
Leu Lys Ile Leu Gln Phe Thr Arg Asn Gly Phe Arg Gln Ile Gly Gln		
	355	360 365
Trp His Val Ala Glu Gly Leu Ser Met Asp Ser His Leu Tyr Ala Ser		
	370	375 380
Asn Ile Ser Asp Thr Leu Phe Asn Thr Thr Leu Val Val Thr Thr Ile		
385	390	395 400
Leu Glu Asn Pro Tyr Leu Met Leu Lys Gly Asn His Gln Glu Met Glu		
	405	410 415
Gly Asn Asp Arg Tyr Glu Gly Phe Cys Val Asp Met Leu Lys Glu Leu		
	420	425 430
Ala Glu Ile Leu Arg Phe Asn Tyr Lys Ile Arg Leu Val Gly Asp Gly		
	435	440 445

Val Tyr Gly Val Pro Glu Ala Asn Gly Thr Trp Thr Gly Met Val Gly  
 450 455 460

Glu Leu Ile Ala Arg Lys Ala Asp Leu Ala Val Ala Gly Leu Thr Ile  
 465 470 475 480

Thr Ala Glu Arg Glu Lys Val Ile Asp Phe Ser Lys Pro Phe Met Thr  
 485 490 495

Leu Gly Ile Ser Ile Leu Tyr Arg Ile His Met Gly Arg Lys Pro Gly  
 500 505 510

Tyr Phe Ser Phe Leu Asp Pro Phe Ser Pro Gly Val Trp Leu Phe Met  
 515 520 525

Leu Leu Ala Tyr Leu Ala Val Ser Cys Val Leu Phe Leu Val Ala Arg  
 530 535 540

Leu Thr Pro Tyr Glu Trp Tyr Ser Pro His Pro Cys Ala Gln Gly Arg  
 545 550 555 560

Cys Asn Leu Leu Val Asn Gln Tyr Ser Leu Gly Asn Ser Leu Trp Phe  
 565 570 575

Pro Val Gly Gly Phe Met Gln Gln Gly Ser Thr Ile Ala Pro Arg Ala  
 580 585 590

Leu Ser Thr Arg Cys Val Ser Gly Val Trp Trp Ala Phe Thr Leu Ile  
 595 600 605

Ile Ile Ser Ser Tyr Thr Ala Asn Leu Ala Ala Phe Leu Thr Val Gln  
 610 615 620

Arg Met Asp Val Pro Ile Glu Ser Val Asp Asp Leu Ala Asp Gln Thr  
 625 630 635 640

Ala Ile Glu Tyr Gly Thr Ile His Gly Gly Ser Ser Met Thr Phe Phe  
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Gln Asn Ser Arg Tyr Gln Thr Tyr Gln Arg Met Trp Asn Tyr Met Tyr  
 660 665 670

Ser Lys Gln Pro Ser Val Phe Val Lys Ser Thr Glu Glu Gly Ile Ala  
 675 680 685

Arg Val Leu Asn Ser Asn Tyr Ala Phe Leu Leu Glu Ser Thr Met Asn  
 690 695 700

Glu Tyr Tyr Arg Gln Arg Asn Cys Asn Leu Thr Gln Ile Gly Gly Leu  
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Leu Asp Thr Lys Gly Tyr Gly Ile Gly Met Pro Val Gly Ser Val Phe  
 725 730 735

Arg Asp Glu Phe Asp Leu Ala Ile Leu Gln Leu Gln Glu Asn Asn Arg  
 740 745 750

Leu Glu Ile Leu Lys Arg Lys Trp Trp Glu Gly Gly Lys Cys Pro Lys  
 755 760 765

Glu Glu Asp His Arg Ala Lys Gly Leu Gly Met Glu Asn Ile Gly Gly  
 770 775 780

Ile Phe Val Val Leu Ile Cys Gly Leu Ile Val Ala Ile Phe Met Ala  
 785 790 795 800

Met Leu Glu Phe Leu Trp Thr Leu Arg His Ser Glu Ala Thr Glu Val  
 805 810 815

Ser Val Cys Gln Glu Met Val Thr Glu Leu Arg Ser Ile Ile Leu Cys  
 820 825 830

Gln Asp Ser Ile His Pro Arg Arg Arg Ala Ala Val Pro Pro Pro  
 835 840 845

Arg Pro Pro Ile Pro Glu Glu Arg Arg Pro Arg Gly Thr Ala Thr Leu  
 850 855 860

Ser Asn Gly Lys Leu Cys Gly Ala Gly Glu Pro Asp Gln Leu Ala Gln  
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Arg Leu Ala Gln Glu Ala Ala Leu Val Ala Arg Gly Cys Thr His Ile  
 885 890 895

Arg Val Cys Pro Glu Cys Arg Arg Phe Gln Gly Leu Arg Ala Arg Pro  
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<212> DNA  
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Pro Leu Pro Ala Ala Ile Thr Ser Gln Leu Asp Lys Ala Ser Ile Ile  
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Arg Leu Thr Ile Ser Tyr Leu Lys Met Arg Asp Phe Ala Asn Gln Gly  
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Asp Pro Pro Trp Asn Leu Arg Met Glu Gly Pro Pro Pro Asn Thr Ser  
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Val Lys Gly Ala Gln Arg Arg Arg Ser Pro Ser Ala Leu Ala Ile Glu  
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Val Phe Glu Ala His Leu Gly Ser His Ile Leu Gln Ser Leu Asp Gly  
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Phe Val Phe Ala Leu Asn Gln Glu Gly Lys Phe Leu Tyr Ile Ser Glu  
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Thr Val Ser Ile Tyr Leu Gly Leu Ser Gln Val Glu Leu Thr Gly Ser  
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Ser Val Phe Asp Tyr Val His Pro Gly Asp His Val Glu Met Ala Glu  
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Gln Leu Gly Met Lys Leu Pro Pro Gly Arg Gly Leu Leu Ser Gln Gly  
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Thr Ala Glu Asp Gly Ala Ser Ser Ala Ser Ser Ser Ser Gln Ser Glu

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Pro Thr Ile Asn Glu Val Arg Ile Asp Cys His Met Phe Val Thr Arg 290 295 300		
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Tyr Met Asp Leu Thr Pro Val Asp Ile Val Gly Lys Arg Cys Tyr His 325 330 335		
Phe Ile His Ala Glu Asp Val Glu Gly Ile Arg His Ser His Leu Asp 340 345 350		
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Lys Asn Gly Gly Tyr Ile Trp Ile Gln Ser Ser Ala Thr Ile Ala Ile 370 375 380		
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Pro His Leu Pro Glu Lys Thr Ser Glu Ser Ser Glu Thr Ser Asp Ser 420 425 430		
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Glu Pro Asp Arg Lys Lys Ser Gly Asn Ala Cys Asp Asn Asp Met Asn  
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Cys Asn Asp Asp Gly His Ser Ser Ser Asn Pro Asp Ser Arg Asp Ser  
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Asp Asp Ser Phe Glu His Ser Asp Phe Glu Asn Pro Lys Ala Gly Glu  
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Asp Gly Phe Gly Ala Leu Gly Ala Met Gln Ile Lys Val Glu Arg Tyr  
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Ala Ser Ser Lys His Gln Lys Arg Lys Lys Arg Arg Lys Arg Gln Lys  
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Gly Leu Asp Ala Gly Leu Val Glu Pro Pro Arg Leu Leu Ser Ser Pro  
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Asn Ser Ala Ser Val Leu Lys Ile Lys Thr Glu Ile Ser Glu Pro Ile  
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Asn Phe Asp Asn Asp Ser Ser Ile Trp Asn Tyr Pro Pro Asn Arg Glu  
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Ile Ser Arg Asn Glu Ser Pro Tyr Ser Met Thr Lys Pro Pro Ser Ser  
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Glu His Phe Pro Ser Pro Gln Gly Gly Gly Gly Gly Gly Gly Gly Gly  
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Ala Asp Gly Ala Ala Ala Arg Lys Thr Gln Phe Gly Ala Ser Ala Thr  
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Ala Ala Leu Ala Pro Val Ala Ser Asp Pro Leu Ser Pro Pro Leu Ser  
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Ala Ser Pro Arg Asp Lys His Pro Gly Asn Gly Gly Gly Gly Gly Gly  
725 730 735

Gly Gly Gly Gly Ala Gly Gly Gly Gly Pro Ser Ala Ser Asn Ser Leu  
740 745 750

Leu Tyr Thr Gly Asp Leu Glu Ala Leu Gln Arg Leu Gln Ala Gly Asn  
755 760 765

Val Val Leu Pro Leu Val His Arg Val Thr Gly Thr Leu Ala Ala Thr  
770 775 780

Ser Thr Ala Ala Gln Arg Val Tyr Thr Thr Gly Thr Ile Arg Tyr Ala  
785 790 795 800

Pro Ala Glu Val Thr Leu Ala Met Gln Ser Asn Leu Leu Pro Asn Ala  
805 810 815

His Ala Val Asn Phe Val Asp Val Asn Ser Pro Gly Phe Gly Leu Asp  
820 825 830

Pro Lys Thr Pro Met Glu Met Leu Tyr His His Val His Arg Leu Asn  
835 840 845

Met Ser Gly Pro Phe Gly Gly Ala Val Ser Ala Ala Ser Leu Thr Gln  
850 855 860

Met Pro Ala Gly Asn Val Phe Thr Thr Ala Glu Gly Leu Phe Ser Thr  
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<400> 54

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Glu Ser Thr Tyr Gln Asn Leu Gln Ala Leu Arg Lys Glu Lys Ser Arg  
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Asp Ala Ala Arg Ser Arg Arg Gly Lys Glu Asn Phe Glu Phe Tyr Glu  
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Leu Ala Lys Leu Leu Pro Leu Pro Ala Ala Ile Thr Ser Gln Leu Asp  
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Lys Ala Ser Ile Ile Arg Leu Thr Ile Ser Tyr Leu Lys Met Arg Asp  
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Phe Ala Asn Gln Gly Asp Pro Pro Trp Asn Leu Arg Met Glu Gly Pro  
 115 120 125

Pro Pro Asn Thr Ser Val Lys Gly Ala Gln Arg Arg Arg Ser Pro Ser  
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Ala Leu Ala Ile Glu Val Phe Glu Ala His Leu Gly Ser His Ile Leu  
 145 150 155 160

Gln Ser Leu Asp Gly Phe Val Phe Ala Leu Asn Gln Glu Gly Lys Phe  
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Leu Tyr Ile Ser Glu Thr Val Ser Ile Tyr Leu Gly Leu Ser Gln Val  
 180 185 190

Glu Leu Thr Gly Ser Ser Val Phe Asp Tyr Val His Pro Gly Asp His  
 195 200 205

Val Glu Met Ala Glu Gln Leu Gly Met Lys Leu Pro Pro Gly Arg Gly  
 210 215 220

Leu Leu Ser Gln Gly Thr Ala Glu Asp Gly Ala Ser Ser Ala Ser Ser  
 225 230 235 240

Ser Ser Gln Ser Glu Thr Pro Glu Pro Val Glu Ser Thr Ser Pro Ser  
 245 250 255

Leu Leu Thr Thr Asp Asn Thr Leu Glu Arg Ser Phe Phe Ile Arg Met  
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Lys Ser Thr Leu Thr Lys Arg Gly Val His Ile Lys Ser Ser Gly Tyr  
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Lys Val Ile His Ile Thr Gly Arg Leu Arg Leu Arg Val Ser Leu Ser

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His Gly Arg Thr Val Pro Ser Gln Ile Met Gly Leu Val Val Val Ala				
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His Ala Leu Pro Pro Pro Thr Ile Asn Glu Val Arg Ile Asp Cys His				
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Met Phe Val Thr Arg Val Asn Met Asp Leu Asn Ile Ile Tyr Cys Glu				
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Asn Arg Ile Ser Asp Tyr Met Asp Leu Thr Pro Val Asp Ile Val Gly				
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Lys Arg Cys Tyr His Phe Ile His Ala Glu Asp Val Glu Gly Ile Arg				
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His Ser His Leu Asp Leu Leu Asn Lys Gly Gln Cys Val Thr Lys Tyr				
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Tyr Arg Trp Met Gln Lys Asn Gly Gly Tyr Ile Trp Ile Gln Ser Ser				
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Ala Thr Ile Ala Ile Asn Ala Lys Asn Ala Asn Glu Lys Asn Ile Ile				
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Trp Val Asn Tyr Leu Leu Ser Asn Pro Glu Tyr Lys Asp Thr Pro Met				
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Asp Ile Ala Gln Leu Pro His Leu Pro Glu Lys Thr Ser Glu Ser Ser				
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Glu Thr Ser Asp Ser Glu Ser Asp Ser Lys Asp Thr Ser Gly Ile Thr				
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Glu Asp Asn Glu Asn Ser Lys Ser Asp Glu Lys Gly Asn Gln Ser Glu				
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Asn Ser Glu Asp Pro Glu Pro Asp Arg Lys Lys Ser Gly Asn Ala Cys				
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Asp Asn Asp Met Asn Cys Asn Asp Asp Gly His Ser Ser Ser Asn Pro				
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Asp Ser Arg Asp Ser Asp Asp Ser Phe Glu His Ser Asp Phe Glu Asn				
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Pro Lys Ala Gly Glu Asp Gly Phe Gly Ala Leu Gly Ala Met Gln Ile  
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Lys Val Glu Arg Tyr Val Glu Ser Glu Ser Asp Leu Arg Leu Gln Asn  
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Cys Glu Ser Leu Thr Ser Asp Ser Ala Lys Asp Ser Asp Ser Ala Gly  
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Glu Ala Gly Ala Gln Ala Ser Ser Lys His Gln Lys Arg Lys Lys Arg  
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Arg Lys Arg Gln Lys Gly Gly Ser Ala Ser Arg Arg Arg Leu Ser Ser  
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Ala Ser Ser Pro Gly Gly Leu Asp Ala Gly Leu Val Glu Pro Pro Arg  
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Leu Leu Ser Ser Pro Asn Ser Ala Ser Val Leu Lys Ile Lys Thr Glu  
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Ile Ser Glu Pro Ile Asn Phe Asp Asn Asp Ser Ser Ile Trp Asn Tyr  
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Pro Pro Asn Arg Glu Ile Ser Arg Asn Glu Ser Pro Tyr Ser Met Thr  
 675 680 685

Lys Pro Pro Ser Ser Glu His Phe Pro Ser Pro Gln Gly Gly Gly Gly  
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Gly Gly Gly Gly Gly Gly Gly Gly Leu His Val Ala Ile Pro Asp Ser Val  
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Leu Thr Pro Pro Gly Ala Asp Gly Ala Ala Ala Arg Lys Thr Gln Phe  
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Gly Ala Ser Ala Thr Ala Ala Leu Ala Pro Val Ala Ser Asp Pro Leu  
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Ser Pro Pro Leu Ser Ala Ser Pro Arg Asp Lys His Pro Gly Asn Gly  
 755 760 765

Gly Gly Gly Gly Gly Gly Gly Gly Gly Ala Gly Gly Gly Gly Pro Ser  
 770 775 780

Ala Ser Asn Ser Leu Leu Tyr Thr Gly Asp Leu Glu Ala Leu Gln Arg  
785 790 795 800

Leu Gln Ala Gly Asn Val Val Leu Pro Leu Val His Arg Val Thr Gly  
805 810 815

Thr Leu Ala Ala Thr Ser Thr Ala Ala Gln Arg Val Tyr Thr Thr Gly  
820 825 830

Thr Ile Arg Tyr Ala Pro Ala Glu Val Thr Leu Ala Met Gln Ser Asn  
835 840 845

Leu Leu Pro Asn Ala His Ala Val Asn Phe Val Asp Val Asn Ser Pro  
850 855 860

Gly Phe Gly Leu Asp Pro Lys Thr Pro Met Glu Met Leu Tyr His His  
865 870 875 880

Val His Arg Leu Asn Met Ser Gly Pro Phe Gly Gly Ala Val Ser Ala  
885 890 895

Ala Ser Leu Thr Gln Met Pro Ala Gly Asn Val Phe Thr Thr Ala Glu  
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Gly Leu Phe Ser Thr Leu Pro Phe Pro Val Tyr Ser Asn Gly Ile His  
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Ala Ala Gln Thr Leu Glu Arg Lys Glu Asp  
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 acagataagc tttcaaagtt gacaaacttt ttgactcct tctggaaaag ggaaagaaaa 2880  
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 gctgtaaaca gaataaaaatt gaacaaatta gggggtagaa aggagcagtg gtgtcgttca 3120  
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 ggccgc 3186

<210> 56  
 <211> 736  
 <212> PRT  
 <213> Homo sapiens

<400> 56

Met Lys Lys Ser Arg Ser Val Met Thr Val Met Ala Asp Asp Asn Val  
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Lys Asp Tyr Phe Glu Cys Ser Leu Ser Lys Ser Tyr Ser Ser Ser Ser  
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Asn Thr Leu Gly Ile Asp Leu Trp Arg Gly Arg Arg Cys Cys Ser Gly  
 35 40 45

Asn Leu Gln Leu Pro Pro Leu Ser Gln Arg Gln Ser Glu Arg Ala Arg  
 50 55 60

Thr Pro Glu Gly Asp Gly Ile Ser Arg Pro Thr Thr Leu Pro Leu Thr  
 65 70 75 80

Thr Leu Pro Ser Ile Ala Ile Thr Thr Val Ser Gln Glu Cys Phe Asp  
 85 90 95  
 Val Glu Asn Gly Pro Ser Pro Gly Arg Ser Pro Leu Asp Pro Gln Ala  
 100 105 110  
 Ser Ser Ser Ala Gly Leu Val Leu His Ala Thr Phe Pro Gly His Ser  
 115 120 125  
 Gln Arg Arg Glu Ser Phe Leu Tyr Arg Ser Asp Ser Asp Tyr Asp Leu  
 130 135 140  
 Ser Pro Lys Ala Met Ser Arg Asn Ser Ser Leu Pro Ser Glu Gln His  
 145 150 155 160  
 Gly Asp Asp Leu Ile Val Thr Pro Phe Ala Gln Val Leu Ala Ser Leu  
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 Arg Ser Val Arg Asn Asn Phe Thr Ile Leu Thr Asn Leu His Gly Thr  
 180 185 190  
 Ser Asn Lys Arg Ser Pro Ala Ala Ser Gln Pro Pro Val Ser Arg Val  
 195 200 205  
 Asn Pro Gln Glu Glu Ser Tyr Gln Lys Leu Ala Met Glu Thr Leu Glu  
 210 215 220  
 Glu Leu Asp Trp Cys Leu Asp Gln Leu Glu Thr Ile Gln Thr Tyr Arg  
 225 230 235 240  
 Ser Val Ser Glu Met Ala Ser Asn Lys Phe Lys Arg Met Leu Asn Arg  
 245 250 255  
 Glu Leu Thr His Leu Ser Glu Met Ser Arg Ser Gly Asn Gln Val Ser  
 260 265 270  
 Glu Tyr Ile Ser Asn Thr Phe Leu Asp Lys Gln Asn Asp Val Glu Ile  
 275 280 285  
 Pro Ser Pro Thr Gln Lys Asp Arg Glu Lys Lys Lys Lys Gln Gln Leu  
 290 295 300  
 Met Thr Gln Ile Ser Gly Val Lys Lys Leu Met His Ser Ser Ser Leu  
 305 310 315 320  
 Asn Asn Thr Ser Ile Ser Arg Phe Gly Val Asn Thr Glu Asn Glu Asp

325	330	335
His Leu Ala Lys Glu Leu Glu Asp Leu Asn Lys Trp Gly Leu Asn Ile		
340	345	350
Phe Asn Val Ala Gly Tyr Ser His Asn Arg Pro Leu Thr Cys Ile Met		
355	360	365
Tyr Ala Ile Phe Gln Glu Arg Asp Leu Leu Lys Thr Phe Arg Ile Ser		
370	375	380
Ser Asp Thr Phe Ile Thr Tyr Met Met Thr Leu Glu Asp His Tyr His		
385	390	395
Ser Asp Val Ala Tyr His Asn Ser Leu His Ala Ala Asp Val Ala Gln		
405	410	415
Ser Thr His Val Leu Leu Ser Thr Pro Ala Leu Asp Ala Val Phe Thr		
420	425	430
Asp Leu Glu Ile Leu Ala Ala Ile Phe Ala Ala Ala Ile His Asp Val		
435	440	445
Asp His Pro Gly Val Ser Asn Gln Phe Leu Ile Asn Thr Asn Ser Glu		
450	455	460
Leu Ala Leu Met Tyr Asn Asp Glu Ser Val Leu Glu Asn His His Leu		
465	470	475
Ala Val Gly Phe Lys Leu Leu Gln Glu Glu His Cys Asp Ile Phe Met		
485	490	495
Asn Leu Thr Lys Lys Gln Arg Gln Thr Leu Arg Lys Met Val Ile Asp		
500	505	510
Met Val Leu Ala Thr Asp Met Ser Lys His Met Ser Leu Leu Ala Asp		
515	520	525
Leu Lys Thr Met Val Glu Thr Lys Lys Val Thr Ser Ser Gly Val Leu		
530	535	540
Leu Leu Asp Asn Tyr Thr Asp Arg Ile Gln Val Leu Arg Asn Met Val		
545	550	555
His Cys Ala Asp Leu Ser Asn Pro Thr Lys Ser Leu Glu Leu Tyr Arg		
565	570	575

Gln Trp Thr Asp Arg Ile Met Glu Glu Phe Phe Gln Gln Gly Asp Lys  
580 585 590

Glu Arg Glu Arg Gly Met Glu Ile Ser Pro Met Cys Asp Lys His Thr  
595 600 605

Ala Ser Val Glu Lys Ser Gln Val Gly Phe Ile Asp Tyr Ile Val His  
610 615 620

Pro Leu Trp Glu Thr Trp Ala Asp Leu Val Gln Pro Asp Ala Gln Asp  
625 630 635 640

Ile Leu Asp Thr Leu Glu Asp Asn Arg Asn Trp Tyr Gln Ser Met Ile  
645 650 655

Pro Gln Ser Pro Ser Pro Pro Leu Asp Glu Gln Asn Arg Asp Cys Gln  
660 665 670

Gly Leu Met Glu Lys Phe Gln Phe Glu Leu Thr Leu Asp Glu Glu Asp  
675 680 685

Ser Glu Gly Pro Glu Lys Glu Gly Glu Gly His Ser Tyr Phe Ser Ser  
690 695 700

Thr Lys Thr Leu Cys Val Ile Asp Pro Glu Asn Arg Asp Ser Leu Gly  
705 710 715 720

Glu Thr Asp Ile Asp Ile Ala Thr Glu Asp Lys Ser Pro Val Asp Thr  
725 730 735

<210> 57  
<211> 2163  
<212> DNA  
<213> Homo sapiens

<400> 57  
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acatctccta aaatttctcc acgcagttca ccaaggaact caccatgctt tttcagaaaag 180  
ttactgggtga ataaaagcat tcggcagcgt cgtcgcttca ctgtggctca tacatgcttt 240  
gatgtggaaa atggcccttc cccaggtcgg agtccactgg atccccaggc cagctcttcc 300  
gctgggctgg tacttcacgc cacctttcct gggcacagcc agcgcagaga gtcatttctc 360  
tacagatcag acagcgacta tgacttgtca ccaaaggcga tgtcgagaaa ctcttctctt 420

ccaagcgagc aacacggcga tgacttgatt gtaactcctt ttgcccaggt ccttgccagc	480
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agggtccccag ctgctagtca gcctcctgtc tccagagtca acccacaaga agaattcttat	600
caaaaattag caatggaaac gctggaggaa ttagactggg gtttagacca gctagagacc	660
atacagacct accggtctgt cagtgagatg gcttctaaca agttcaaaag aatgctgaac	720
cgggagctga cacacctctc agagatgagc cgatcaggga accaggtgtc tgaatacatt	780
tcaaatactt tcttagacaa gcagaatgat gtggagatcc catctcctac ccagaaagac	840
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catagttcaa gcctaaacaa tacaagcatc tcacgctttg gagtcaacac tgaaaatgaa	960
gatcacctgg ccaaggagct ggaagacctg aacaaatggg gtcttaacat ctttaatgtg	1020
gctggatatt ctcaaatag acccctaaca tgcacatgt atgctatatt ccaggaaaga	1080
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gcaactgata tgtctaaaca tatgagcctg ctggcagacc tgaagacaat ggtagaaacg	1560
aagaaagtta caagttcagg cgttcttctc ctagacaact ataccgatcg cattcaggtc	1620
cttcgcaaca tggtagactg tgcagacctg agcaacccca ccaagtcctt ggaattgtat	1680
cggcaatgga cagaccgcat catggaggaa tttttccagc agggagacaa agagcgggag	1740
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cctgatgctc aggacattct cgatacctta gaagataaca ggaactggta tcagagcatg	1920
atacctcaaa gtccctcacc accactggac gagcagaaca gggactgccca gggctctgatg	1980
gagaagtttc agtttgaact gactctcgat gaggaagatt ctgaaggacc tgagaaggag	2040
ggagagggac acagctatct cagcagcaca aagacgcttt gtgtgattga tccagaaaac	2100
agagattccc tgggagagac tgacatagac attgcaacag aagacaagtc ccccgtagat	2160
aca	2163

<210> 58  
 <211> 721  
 <212> PRT  
 <213> Homo sapiens

<400> 58

Met Thr Ala Lys Asp Ser Ser Lys Glu Leu Thr Ala Ser Glu Pro Glu  
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Val Cys Ile Lys Thr Phe Lys Glu Gln Met His Leu Glu Leu Glu Leu  
 20 25 30

Pro Arg Leu Pro Gly Asn Arg Pro Thr Ser Pro Lys Ile Ser Pro Arg  
 35 40 45

Ser Ser Pro Arg Asn Ser Pro Cys Phe Phe Arg Lys Leu Leu Val Asn  
 50 55 60

Lys Ser Ile Arg Gln Arg Arg Arg Phe Thr Val Ala His Thr Cys Phe  
 65 70 75 80

Asp Val Glu Asn Gly Pro Ser Pro Gly Arg Ser Pro Leu Asp Pro Gln  
 85 90 95

Ala Ser Ser Ser Ala Gly Leu Val Leu His Ala Thr Phe Pro Gly His  
 100 105 110

Ser Gln Arg Arg Glu Ser Phe Leu Tyr Arg Ser Asp Ser Asp Tyr Asp  
 115 120 125

Leu Ser Pro Lys Ala Met Ser Arg Asn Ser Ser Leu Pro Ser Glu Gln  
 130 135 140

His Gly Asp Asp Leu Ile Val Thr Pro Phe Ala Gln Val Leu Ala Ser  
 145 150 155 160

Leu Arg Ser Val Arg Asn Asn Phe Thr Ile Leu Thr Asn Leu His Gly  
 165 170 175

Thr Ser Asn Lys Arg Ser Pro Ala Ala Ser Gln Pro Pro Val Ser Arg  
 180 185 190

Val Asn Pro Gln Glu Glu Ser Tyr Gln Lys Leu Ala Met Glu Thr Leu  
 195 200 205

Glu Glu Leu Asp Trp Cys Leu Asp Gln Leu Glu Thr Ile Gln Thr Tyr

210	215	220
Arg Ser Val Ser Glu Met Ala Ser Asn Lys Phe Lys Arg Met Leu Asn		
225	230	235 240
Arg Glu Leu Thr His Leu Ser Glu Met Ser Arg Ser Gly Asn Gln Val		
	245	250 255
Ser Glu Tyr Ile Ser Asn Thr Phe Leu Asp Lys Gln Asn Asp Val Glu		
	260	265 270
Ile Pro Ser Pro Thr Gln Lys Asp Arg Glu Lys Lys Lys Lys Gln Gln		
	275	280 285
Leu Met Thr Gln Ile Ser Gly Val Lys Lys Leu Met His Ser Ser Ser		
	290	295 300
Leu Asn Asn Thr Ser Ile Ser Arg Phe Gly Val Asn Thr Glu Asn Glu		
305	310	315 320
Asp His Leu Ala Lys Glu Leu Glu Asp Leu Asn Lys Trp Gly Leu Asn		
	325	330 335
Ile Phe Asn Val Ala Gly Tyr Ser His Asn Arg Pro Leu Thr Cys Ile		
	340	345 350
Met Tyr Ala Ile Phe Gln Glu Arg Asp Leu Leu Lys Thr Phe Arg Ile		
	355	360 365
Ser Ser Asp Thr Phe Ile Thr Tyr Met Met Thr Leu Glu Asp His Tyr		
	370	375 380
His Ser Asp Val Ala Tyr His Asn Ser Leu His Ala Ala Asp Val Ala		
385	390	395 400
Gln Ser Thr His Val Leu Leu Ser Thr Pro Ala Leu Asp Ala Val Phe		
	405	410 415
Thr Asp Leu Glu Ile Leu Ala Ala Ile Phe Ala Ala Ala Ile His Asp		
	420	425 430
Val Asp His Pro Gly Val Ser Asn Gln Phe Leu Ile Asn Thr Asn Ser		
	435	440 445
Glu Leu Ala Leu Met Tyr Asn Asp Glu Ser Val Leu Glu Asn His His		
450	455	460



Leu Ala Val Gly Phe Lys Leu Leu Gln Glu Glu His Cys Asp Ile Phe  
 465 470 475 480

Met Asn Leu Thr Lys Lys Gln Arg Gln Thr Leu Arg Lys Met Val Ile  
 485 490 495

Asp Met Val Leu Ala Thr Asp Met Ser Lys His Met Ser Leu Leu Ala  
 500 505 510

Asp Leu Lys Thr Met Val Glu Thr Lys Lys Val Thr Ser Ser Gly Val  
 515 520 525

Leu Leu Leu Asp Asn Tyr Thr Asp Arg Ile Gln Val Leu Arg Asn Met  
 530 535 540

Val His Cys Ala Asp Leu Ser Asn Pro Thr Lys Ser Leu Glu Leu Tyr  
 545 550 555 560

Arg Gln Trp Thr Asp Arg Ile Met Glu Glu Phe Phe Gln Gln Gly Asp  
 565 570 575

Lys Glu Arg Glu Arg Gly Met Glu Ile Ser Pro Met Cys Asp Lys His  
 580 585 590

Thr Ala Ser Val Glu Lys Ser Gln Val Gly Phe Ile Asp Tyr Ile Val  
 595 600 605

His Pro Leu Trp Glu Thr Trp Ala Asp Leu Val Gln Pro Asp Ala Gln  
 610 615 620

Asp Ile Leu Asp Thr Leu Glu Asp Asn Arg Asn Trp Tyr Gln Ser Met  
 625 630 635 640

Ile Pro Gln Ser Pro Ser Pro Pro Leu Asp Glu Gln Asn Arg Asp Cys  
 645 650 655

Gln Gly Leu Met Glu Lys Phe Gln Phe Glu Leu Thr Leu Asp Glu Glu  
 660 665 670

Asp Ser Glu Gly Pro Glu Lys Glu Gly Glu Gly His Ser Tyr Phe Ser  
 675 680 685

Ser Thr Lys Thr Leu Cys Val Ile Asp Pro Glu Asn Arg Asp Ser Leu  
 690 695 700

Gly Glu Thr Asp Ile Asp Ile Ala Thr Glu Asp Lys Ser Pro Val Asp  
 705 710 715 720

Thr

<210> 59  
 <211> 4068  
 <212> DNA  
 <213> Homo sapiens

<400> 59  
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 gtatataatg taatgttttg taagttatta atttatatat ctaacattgc ctgccaatgg 180  
 tgggtgttaaa tttgtgtaga aaactctgcc taagagttac gactttttct tgtaatgttt 240  
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 cgggggggttg gggggaaact tggcaccagc catcccaggc agagcaccac tgtgatttgt 720  
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 cagccgctcc agcctaacta catgcctgtg tgtttgtttg cagaagaatc ttatcaaaaa 900  
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agaataaaaat	tgaacaaatt	agggggtaga	aaggagcagt	ggtgtcgttc	accgtgagag	3240

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<210> 60  
<211> 564  
<212> PRT  
<213> Homo sapiens

<400> 60

Met Lys Glu His Gly Gly Thr Phe Ser Ser Thr Gly Ile Ser Gly Gly  
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Ser Gly Asp Ser Ala Met Asp Ser Leu Gln Pro Leu Gln Pro Asn Tyr  
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Met Pro Val Cys Leu Phe Ala Glu Glu Ser Tyr Gln Lys Leu Ala Met  
35 40 45

Glu Thr Leu Glu Glu Leu Asp Trp Cys Leu Asp Gln Leu Glu Thr Ile  
50 55 60

Gln Thr Tyr Arg Ser Val Ser Glu Met Ala Ser Asn Lys Phe Lys Arg  
65 70 75 80

Met Leu Asn Arg Glu Leu Thr His Leu Ser Glu Met Ser Arg Ser Gly  
85 90 95

Asn	Gln	Val	Ser	Glu	Tyr	Ile	Ser	Asn	Thr	Phe	Leu	Asp	Lys	Gln	Asn	
			100					105					110			
Asp	Val	Glu	Ile	Pro	Ser	Pro	Thr	Gln	Lys	Asp	Arg	Glu	Lys	Lys	Lys	
		115					120					125				
Lys	Gln	Gln	Leu	Met	Thr	Gln	Ile	Ser	Gly	Val	Lys	Lys	Leu	Met	His	
	130					135					140					
Ser	Ser	Ser	Leu	Asn	Asn	Thr	Ser	Ile	Ser	Arg	Phe	Gly	Val	Asn	Thr	
145					150					155					160	
Glu	Asn	Glu	Asp	His	Leu	Ala	Lys	Glu	Leu	Glu	Asp	Leu	Asn	Lys	Trp	
				165					170					175		
Gly	Leu	Asn	Ile	Phe	Asn	Val	Ala	Gly	Tyr	Ser	His	Asn	Arg	Pro	Leu	
		180						185					190			
Thr	Cys	Ile	Met	Tyr	Ala	Ile	Phe	Gln	Glu	Arg	Asp	Leu	Leu	Lys	Thr	
		195					200					205				
Phe	Arg	Ile	Ser	Ser	Asp	Thr	Phe	Ile	Thr	Tyr	Met	Met	Thr	Leu	Glu	
	210					215					220					
Asp	His	Tyr	His	Ser	Asp	Val	Ala	Tyr	His	Asn	Ser	Leu	His	Ala	Ala	
225					230					235					240	
Asp	Val	Ala	Gln	Ser	Thr	His	Val	Leu	Leu	Ser	Thr	Pro	Ala	Leu	Asp	
				245					250					255		
Ala	Val	Phe	Thr	Asp	Leu	Glu	Ile	Leu	Ala	Ala	Ile	Phe	Ala	Ala	Ala	
			260					265					270			
Ile	His	Asp	Val	Asp	His	Pro	Gly	Val	Ser	Asn	Gln	Phe	Leu	Ile	Asn	
		275					280					285				
Thr	Asn	Ser	Glu	Leu	Ala	Leu	Met	Tyr	Asn	Asp	Glu	Ser	Val	Leu	Glu	
	290					295					300					
Asn	His	His	Leu	Ala	Val	Gly	Phe	Lys	Leu	Leu	Gln	Glu	Glu	His	Cys	
305				310						315					320	
Asp	Ile	Phe	Met	Asn	Leu	Thr	Lys	Lys	Gln	Arg	Gln	Thr	Leu	Arg	Lys	
				325					330					335		
Met	Val	Ile	Asp	Met	Val	Leu	Ala	Thr	Asp	Met	Ser	Lys	His	Met	Ser	

340	345	350
Leu Leu Ala Asp Leu Lys Thr Met Val Glu Thr Lys Lys Val Thr Ser		
355	360	365
Ser Gly Val Leu Leu Leu Asp Asn Tyr Thr Asp Arg Ile Gln Val Leu		
370	375	380
Arg Asn Met Val His Cys Ala Asp Leu Ser Asn Pro Thr Lys Ser Leu		
385	390	400
Glu Leu Tyr Arg Gln Trp Thr Asp Arg Ile Met Glu Glu Phe Phe Gln		
	405	410
		415
Gln Gly Asp Lys Glu Arg Glu Arg Gly Met Glu Ile Ser Pro Met Cys		
	420	425
		430
Asp Lys His Thr Ala Ser Val Glu Lys Ser Gln Val Gly Phe Ile Asp		
	435	440
		445
Tyr Ile Val His Pro Leu Trp Glu Thr Trp Ala Asp Leu Val Gln Pro		
	450	455
		460
Asp Ala Gln Asp Ile Leu Asp Thr Leu Glu Asp Asn Arg Asn Trp Tyr		
465	470	475
		480
Gln Ser Met Ile Pro Gln Ser Pro Ser Pro Pro Leu Asp Glu Gln Asn		
	485	490
		495
Arg Asp Cys Gln Gly Leu Met Glu Lys Phe Gln Phe Glu Leu Thr Leu		
	500	505
		510
Asp Glu Glu Asp Ser Glu Gly Pro Glu Lys Glu Gly Glu Gly His Ser		
	515	520
		525
Tyr Phe Ser Ser Thr Lys Thr Leu Cys Val Ile Asp Pro Glu Asn Arg		
	530	535
		540
Asp Ser Leu Gly Glu Thr Asp Ile Asp Ile Ala Thr Glu Asp Lys Ser		
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		560
Pro Val Asp Thr		

<210> 61  
 <211> 2929

<212> DNA  
 <213> Homo sapiens

<400> 61  
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 caatgaaaag aaaagccaat ggattgtggt cttagaaaag ctgcttagat gatgtctggt 120  
 tcccgTgcta tagacacgtg gcagagctgt aagtaaTgc tcggcactgc atgatgaatt 180  
 ggatggctgc agaccggaga caaaaaaat aattgtctca ttttcgtggt gatttgctta 240  
 actggtggga ccatgccaga acggctagcg gaaatgctct tggatctctg gactccatta 300  
 ataatattat ggattactct tcccccttgc atttacatgg ctccgatgaa tcagtctcaa 360  
 gttttaatga gtggatcccc tttggaacta aacagtctgg gtgaagaaca gcgaattttg 420  
 aaccgctcca aaagaggctg ggtttggaat caaatgtttg tcctggaaga gttttctgga 480  
 cctgaaccga ttcttggttg ccggctacac acagacctgg atcctgggag caaaaaaatc 540  
 aagtatatcc tatcaggTga tggagctggg accatatTtc aaataaatga tgtaactgga 600  
 gatatccatg ctataaaaag acttgaccgg gaggaaaagg ctgagtatac cctaacagct 660  
 caagcagtgg actgggagac aagcaaact ctggagcctc cttctgaatt tattattaaa 720  
 gttcaagaca tcaatgacaa tgcaccagag tttcttaatg gacctatca tgctactgtg 780  
 ccagaaatgt ccattttggg tacatctgtc actaacgtca ctgogaccga cgctgatgac 840  
 ccagtttatg gaaacagtgc aaagtTggtt tatagtatat tgggaagggca gccttatttt 900  
 tccattgagc ctgaaacagc tattataaaa actgcccttc ccaacatgga cagagaagcc 960  
 aaggaggagt acctggttgt tatccaagcc aaagatatgg gtggacactc tggTggcctg 1020  
 tctgggacca cgacacttac agtgactctt actgatgtta atgacaatcc tccaaaatTT 1080  
 gcacagagcc tgtatcactt ctcagtaccg gaagatgtgg ttcttggcac tgcaatagga 1140  
 agggTgaagg ccaatgatca ggatattggt gaaaatgcac agtcatcata tgatatcatc 1200  
 gatggagatg gaacagcact ttttgaaatc acttctgatg ccagggccca ggatggcatt 1260  
 ataaggctaa gaaaacctct ggactttgag accaaaaaat cctatacgct aaaggtagag 1320  
 gcagccaatg tccatattga ccacgcttc agtggcaggg ggccctttaa agacacggcg 1380  
 acagtcaaaa tcgtggttga agatgctgat gagcctccgg tcttctcttc accgacttac 1440  
 ctacttgaag ttcatgaaaa tgctgctcta aactccgtga ttgggcaagt gactgctcgt 1500  
 gacctgata tcacttccag tcctataagg ttttccatcg accggcacac tgacctggag 1560  
 aggcagttca acattaatgc agacgatggg aagataacgc tggcaacacc acttgacaga 1620  
 gaattaagtg tatggcacia cataacaatc attgctactg aaattaggaa ccacagtcag 1680  
 atatcacgag tacctgttgc tattaagtg ctggatgtca atgacaacgc ccctgaattc 1740

gcatccgaat atgaggcatt tttatgtgaa aatggaaaac cgggccaagt cattcaaact 1800  
 gttagcgcca tggacaaaga tgatcccaaa aacggacatt atttcttata cagtctcctt 1860  
 ccagaaatgg tcaacaatcc gaatttcacc atcaagaaaa atgaagataa ttccctcagt 1920  
 attttggcaa agcataatgg attcaaccgc cagaagcaag aagtctatct tttaccaatc 1980  
 ataatcagtg atagtggaaa tctccactg agcagcacta gcaccttgac aatcagggtc 2040  
 tgtggctgca gcaatgacgg tgcgtccag tcttgcaatg tcgaagctta tgccttcca 2100  
 attggactca gtatgggccc cttaattgcc atattagcat gcatcatttt gctgttagtc 2160  
 atcgtggtgc tgtttgtaac tctacggcgg cataaaaatg aaccattaat tatcaaagat 2220  
 gatgaagacg ttcgagaaaa catcattcgc tacgatgatg aaggaggagg ggaggaggac 2280  
 acagaggctt ttgacattgc aactttacaa aatccagatg gaattaatgg atttttaccc 2340  
 cgtaaggata ttaaaccaga tttgcagttt atgccaaaggc aagggttgc tccagttcca 2400  
 aatggtgttg atgtcgatga atttataaat gtaaggctgc atgaggcaga taatgatccc 2460  
 acggccccgc catatgactc cattcagata tatggctatg aaggccgagg gtcagtggct 2520  
 ggctccctca gtccttggg gtccaccaca tcagactcag accagaattt tgactacctc 2580  
 agtgactggg gtccccgctt taagagactg ggcgaactct actctgttgg tgaaagtgc 2640  
 aaagaaactt gacagtggat tataaataaa tcaactggaac tgagcattct gtaatatctt 2700  
 agggtcactc cccttagata caaccaatgt ggctatttgt tttagaggca agtttagcac 2760  
 cagtcactta taaactcaac cacattttta tgttgaacca aaaaagata ataaaataaa 2820  
 aaagtatatg ttaggaggtt ataaatcttg tggagtgtga attaagtatg tggagtgtct 2880  
 agaagtcctt ggatatttga tatttacctg accaccacag acaaagatt 2929

<210> 62  
 <211> 799  
 <212> PRT  
 <213> Homo sapiens

<400> 62

Met Pro Glu Arg Leu Ala Glu Met Leu Leu Asp Leu Trp Thr Pro Leu  
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Ile Ile Leu Trp Ile Thr Leu Pro Pro Cys Ile Tyr Met Ala Pro Met  
 20 25 30

Asn Gln Ser Gln Val Leu Met Ser Gly Ser Pro Leu Glu Leu Asn Ser  
 35 40 45



Leu Gly Glu Glu Gln Arg Ile Leu Asn Arg Ser Lys Arg Gly Trp Val  
 50 55 60

Trp Asn Gln Met Phe Val Leu Glu Glu Phe Ser Gly Pro Glu Pro Ile  
 65 70 75 80

Leu Val Gly Arg Leu His Thr Asp Leu Asp Pro Gly Ser Lys Lys Ile  
 85 90 95

Lys Tyr Ile Leu Ser Gly Asp Gly Ala Gly Thr Ile Phe Gln Ile Asn  
 100 105 110

Asp Val Thr Gly Asp Ile His Ala Ile Lys Arg Leu Asp Arg Glu Glu  
 115 120 125

Lys Ala Glu Tyr Thr Leu Thr Ala Gln Ala Val Asp Trp Glu Thr Ser  
 130 135 140

Lys Pro Leu Glu Pro Pro Ser Glu Phe Ile Ile Lys Val Gln Asp Ile  
 145 150 155 160

Asn Asp Asn Ala Pro Glu Phe Leu Asn Gly Pro Tyr His Ala Thr Val  
 165 170 175

Pro Glu Met Ser Ile Leu Gly Thr Ser Val Thr Asn Val Thr Ala Thr  
 180 185 190

Asp Ala Asp Asp Pro Val Tyr Gly Asn Ser Ala Lys Leu Val Tyr Ser  
 195 200 205

Ile Leu Glu Gly Gln Pro Tyr Phe Ser Ile Glu Pro Glu Thr Ala Ile  
 210 215 220

Ile Lys Thr Ala Leu Pro Asn Met Asp Arg Glu Ala Lys Glu Glu Tyr  
 225 230 235 240

Leu Val Val Ile Gln Ala Lys Asp Met Gly Gly His Ser Gly Gly Leu  
 245 250 255

Ser Gly Thr Thr Thr Leu Thr Val Thr Leu Thr Asp Val Asn Asp Asn  
 260 265 270

Pro Pro Lys Phe Ala Gln Ser Leu Tyr His Phe Ser Val Pro Glu Asp  
 275 280 285

Val Val Leu Gly Thr Ala Ile Gly Arg Val Lys Ala Asn Asp Gln Asp

290		295		300
Ile Gly Glu Asn Ala Gln Ser Ser Tyr Asp	Ile Ile Asp Gly Asp Gly			
305	310	315	320	
Thr Ala Leu Phe Glu Ile Thr Ser Asp Ala Gln Ala Gln Asp Gly Ile				
	325	330	335	
Ile Arg Leu Arg Lys Pro Leu Asp Phe Glu Thr Lys Lys Ser Tyr Thr				
	340	345	350	
Leu Lys Val Glu Ala Ala Asn Val His Ile Asp Pro Arg Phe Ser Gly				
	355	360	365	
Arg Gly Pro Phe Lys Asp Thr Ala Thr Val Lys Ile Val Val Glu Asp				
	370	375	380	
Ala Asp Glu Pro Pro Val Phe Ser Ser Pro Thr Tyr Leu Leu Glu Val				
385	390	395	400	
His Glu Asn Ala Ala Leu Asn Ser Val Ile Gly Gln Val Thr Ala Arg				
	405	410	415	
Asp Pro Asp Ile Thr Ser Ser Pro Ile Arg Phe Ser Ile Asp Arg His				
	420	425	430	
Thr Asp Leu Glu Arg Gln Phe Asn Ile Asn Ala Asp Asp Gly Lys Ile				
	435	440	445	
Thr Leu Ala Thr Pro Leu Asp Arg Glu Leu Ser Val Trp His Asn Ile				
	450	455	460	
Thr Ile Ile Ala Thr Glu Ile Arg Asn His Ser Gln Ile Ser Arg Val				
465	470	475	480	
Pro Val Ala Ile Lys Val Leu Asp Val Asn Asp Asn Ala Pro Glu Phe				
	485	490	495	
Ala Ser Glu Tyr Glu Ala Phe Leu Cys Glu Asn Gly Lys Pro Gly Gln				
	500	505	510	
Val Ile Gln Thr Val Ser Ala Met Asp Lys Asp Asp Pro Lys Asn Gly				
	515	520	525	
His Tyr Phe Leu Tyr Ser Leu Leu Pro Glu Met Val Asn Asn Pro Asn				
	530	535	540	

Phe Thr Ile Lys Lys Asn Glu Asp Asn Ser Leu Ser Ile Leu Ala Lys  
545 550 555 560

His Asn Gly Phe Asn Arg Gln Lys Gln Glu Val Tyr Leu Leu Pro Ile  
565 570 575

Ile Ile Ser Asp Ser Gly Asn Pro Pro Leu Ser Ser Thr Ser Thr Leu  
580 585 590

Thr Ile Arg Val Cys Gly Cys Ser Asn Asp Gly Val Val Gln Ser Cys  
595 600 605

Asn Val Glu Ala Tyr Val Leu Pro Ile Gly Leu Ser Met Gly Ala Leu  
610 615 620

Ile Ala Ile Leu Ala Cys Ile Ile Leu Leu Leu Val Ile Val Val Leu  
625 630 635 640

Phe Val Thr Leu Arg Arg His Lys Asn Glu Pro Leu Ile Ile Lys Asp  
645 650 655

Asp Glu Asp Val Arg Glu Asn Ile Ile Arg Tyr Asp Asp Glu Gly Gly  
660 665 670

Gly Glu Glu Asp Thr Glu Ala Phe Asp Ile Ala Thr Leu Gln Asn Pro  
675 680 685

Asp Gly Ile Asn Gly Phe Leu Pro Arg Lys Asp Ile Lys Pro Asp Leu  
690 695 700

Gln Phe Met Pro Arg Gln Gly Leu Ala Pro Val Pro Asn Gly Val Asp  
705 710 715 720

Val Asp Glu Phe Ile Asn Val Arg Leu His Glu Ala Asp Asn Asp Pro  
725 730 735

Thr Ala Pro Pro Tyr Asp Ser Ile Gln Ile Tyr Gly Tyr Glu Gly Arg  
740 745 750

Gly Ser Val Ala Gly Ser Leu Ser Ser Leu Glu Ser Thr Thr Ser Asp  
755 760 765

Ser Asp Gln Asn Phe Asp Tyr Leu Ser Asp Trp Gly Pro Arg Phe Lys  
770 775 780

Arg Leu Gly Glu Leu Tyr Ser Val Gly Glu Ser Asp Lys Glu Thr  
 785 790 795

<210> 63  
 <211> 93  
 <212> PRT  
 <213> Homo sapiens  
 <400> 63

Met Pro Glu Arg Leu Ala Glu Met Leu Leu Asp Leu Trp Thr Pro Leu  
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Ile Ile Leu Trp Ile Thr Leu Pro Pro Cys Ile Tyr Met Ala Pro Met  
 20 25 30

Asn Gln Ser Gln Val Leu Met Ser Gly Ser Pro Leu Glu Leu Asn Ser  
 35 40 45

Leu Gly Glu Glu Gln Arg Ile Leu Asn Arg Ser Lys Arg Gly Trp Val  
 50 55 60

Trp Asn Gln Met Phe Val Leu Glu Glu Phe Ser Gly Pro Glu Pro Ile  
 65 70 75 80

Leu Val Gly Arg Val Leu Lys Ser Val Ser Lys Leu His  
 85 90

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 <212> DNA  
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 gatggagctg ggaccatatt tcaaataaat gatgtaactg gagatatcca tgctataaaa 180  
 agacttgacc gggaggaaaa ggctgagtat accctaacag ctcaagcagt ggactgggag 240  
 acaagcaaac ctctggagcc tccttctgaa tttattatta aagttcaaga catcaatgac 300  
 aatgcaccag agtttcttaa tggaccctat catgctactg tgccagaaat gtccattttg 360  
 ggtacatctg tactaactg cactgcgacc gacgctgatg acccagttta tggaaacagt 420  
 gcaaagttgg tttatagtat attggaaggg cagccttatt tttccattga gcctgaaaca 480  
 gctattataa aaactgcctt tcccaacatg gacagagaag ccaaggagga gtacctgggt 540  
 gttatccaag ccaaagatat ggggtggacac tctggtggcc tgtctgggac cacgacactt 600

acagtgactc ttactgatgt taatgacaat cctccaaaat ttgcacagag cctgtatcac 660  
 ttctcagtag cggaagatgt ggttcttggc actgcaatag gaagggtgaa ggccaatgat 720  
 caggatattg gtgaaaatgc acagtcacatca tatgatataca tcgatggaga tggaacagca 780  
 ctttttgaaa tcacttctga tgcccaggcc caggatggca ttataaggct aagaaaacct 840  
 ctggactttg agaccacaaaa atcctatacg ctaaaggtag aggcagccaa tgtccatatt 900  
 gacccacgct tcagtggcag ggggcccttt aaagacacgg cgacagtcaa aatcgtggtt 960  
 gaagatgctg atgagcctcc ggtcttctct tcaccgactt acctacttga agttcatgaa 1020  
 aatgctgctc taaactccgt gattgggcaa gtgactgctc gt 1062

<210> 65  
 <211> 354  
 <212> PRT  
 <213> Homo sapiens

<400> 65

Gly Arg Gly Gly Ala Ala Glu Ala Pro Arg Ala Gly Gly Gly Arg Leu  
 1 5 10 15

Leu Arg Gly Gln Pro Glu Leu His Thr Asp Leu Asp Pro Gly Ser Lys  
 20 25 30

Lys Ile Lys Tyr Ile Leu Ser Gly Asp Gly Ala Gly Thr Ile Phe Gln  
 35 40 45

Ile Asn Asp Val Thr Gly Asp Ile His Ala Ile Lys Arg Leu Asp Arg  
 50 55 60

Glu Glu Lys Ala Glu Tyr Thr Leu Thr Ala Gln Ala Val Asp Trp Glu  
 65 70 75 80

Thr Ser Lys Pro Leu Glu Pro Pro Ser Glu Phe Ile Ile Lys Val Gln  
 85 90 95

Asp Ile Asn Asp Asn Ala Pro Glu Phe Leu Asn Gly Pro Tyr His Ala  
 100 105 110

Thr Val Pro Glu Met Ser Ile Leu Gly Thr Ser Val Thr Asn Val Thr  
 115 120 125

Ala Thr Asp Ala Asp Asp Pro Val Tyr Gly Asn Ser Ala Lys Leu Val  
 130 135 140

Tyr Ser Ile Leu Glu Gly Gln Pro Tyr Phe Ser Ile Glu Pro Glu Thr  
 145 150 155 160  
 Ala Ile Ile Lys Thr Ala Leu Pro Asn Met Asp Arg Glu Ala Lys Glu  
 165 170 175  
 Glu Tyr Leu Val Val Ile Gln Ala Lys Asp Met Gly Gly His Ser Gly  
 180 185 190  
 Gly Leu Ser Gly Thr Thr Thr Leu Thr Val Thr Leu Thr Asp Val Asn  
 195 200 205  
 Asp Asn Pro Pro Lys Phe Ala Gln Ser Leu Tyr His Phe Ser Val Pro  
 210 215 220  
 Glu Asp Val Val Leu Gly Thr Ala Ile Gly Arg Val Lys Ala Asn Asp  
 225 230 235 240  
 Gln Asp Ile Gly Glu Asn Ala Gln Ser Ser Tyr Asp Ile Ile Asp Gly  
 245 250 255  
 Asp Gly Thr Ala Leu Phe Glu Ile Thr Ser Asp Ala Gln Ala Gln Asp  
 260 265 270  
 Gly Ile Ile Arg Leu Arg Lys Pro Leu Asp Phe Glu Thr Lys Lys Ser  
 275 280 285  
 Tyr Thr Leu Lys Val Glu Ala Ala Asn Val His Ile Asp Pro Arg Phe  
 290 295 300  
 Ser Gly Arg Gly Pro Phe Lys Asp Thr Ala Thr Val Lys Ile Val Val  
 305 310 315 320  
 Glu Asp Ala Asp Glu Pro Pro Val Phe Ser Ser Pro Thr Tyr Leu Leu  
 325 330 335  
 Glu Val His Glu Asn Ala Ala Leu Asn Ser Val Ile Gly Gln Val Thr  
 340 345 350

Ala Arg

<210> 66  
 <211> 20  
 <212> DNA  
 <213> ARTIFICIAL SEQUENCE

<220>  
 <223> OLIGONUCLEOTIDE  
  
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 <210> 67  
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 <212> DNA  
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 <223> OLIGONUCLEOTIDE  
  
 <400> 67  
 tgcctttaac cagatgaggc 20  
  
 <210> 68  
 <211> 21  
 <212> DNA  
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 <400> 68  
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 <210> 69  
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 <400> 69  
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 <210> 70  
 <211> 23  
 <212> DNA  
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 <400> 70  
 aaatgaatct ctgattagcc aac 23  
  
 <210> 71  
 <211> 22  
 <212> DNA  
 <213> ARTIFICIAL SEQUENCE  
  
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<223> OLIGONUCLEOTIDE  
 <400> 71  
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<210> 72  
 <211> 20  
 <212> DNA  
 <213> ARTIFICIAL SEQUENCE

<220>  
 <223> OLIGONUCLEOTIDE  
 <400> 72  
 aggctgagtg ccaaaaagta 20

<210> 73  
 <211> 23  
 <212> DNA  
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<220>  
 <223> OLIGONUCLEOTIDE  
 <400> 73  
 ctttaagctt gctatttgaa ggc 23

<210> 74  
 <211> 18  
 <212> DNA  
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<220>  
 <223> OLIGONUCLEOTIDE  
 <400> 74  
 ttcacgtct gaacctgg 18

<210> 75  
 <211> 20  
 <212> DNA  
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<220>  
 <223> OLIGONUCLEOTIDE  
 <400> 75  
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<210> 76  
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<220>  
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<400> 77		
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<210> 78		
<211> 20		
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<210> 79		
<211> 20		
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<223> OLIGONUCLEOTIDE		
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<210> 80		
<211> 20		
<212> DNA		
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<220>		
<223> OLIGONUCLEOTIDE		
<400> 80		
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<210> 81		
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<212> DNA		
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<400> 81	
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<400> 82	
ttgaacccaa gagaacaggg	20
<210> 83	
<211> 20	
<212> DNA	
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<223> OLIGONUCLEOTIDE	
<400> 83	
tccccttctc cttccagttt	20
<210> 84	
<211> 20	
<212> DNA	
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<220>	
<223> OLIGONUCLEOTIDE	
<400> 84	
acaaccattc tgggaacagc	20
<210> 85	
<211> 20	
<212> DNA	
<213> ARTIFICIAL SEQUENCE	
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<223> OLIGONUCLEOTIDE	
<400> 85	
gtgtagggaa agccatccaa	20
<210> 86	
<211> 20	
<212> DNA	
<213> ARTIFICIAL SEQUENCE	
<220>	
<223> OLIGONUCLEOTIDE	
<400> 86	

tcttttttcct gcagtcacctg	20
<210> 87	
<211> 20	
<212> DNA	
<213> ARTIFICIAL SEQUENCE	
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<400> 87	
ctccaaatga ctcttgccat	20
<210> 88	
<211> 20	
<212> DNA	
<213> ARTIFICIAL SEQUENCE	
<220>	
<223> OLIGONUCLEOTIDE	
<400> 88	
gcctctgcca tagattttgc	20
<210> 89	
<211> 20	
<212> DNA	
<213> ARTIFICIAL SEQUENCE	
<220>	
<223> OLIGONUCLEOTIDE	
<400> 89	
ttccttccca ccctttctct	20
<210> 90	
<211> 20	
<212> DNA	
<213> ARTIFICIAL SEQUENCE	
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<223> OLIGONUCLEOTIDE	
<400> 90	
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<210> 91	
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<223> OLIGONUCLEOTIDE	
<400> 91	
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<210> 92  
<211> 23  
<212> DNA  
<213> ARTIFICIAL SEQUENCE

<220>  
<223> OLIGONUCLEOTIDE

<400> 92  
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23

<210> 93  
<211> 23  
<212> DNA  
<213> ARTIFICIAL SEQUENCE

<220>  
<223> OLIGONUCLEOTIDE

<400> 93  
ctttctcctg tcactttcct tca

23

<210> 94  
<211> 9  
<212> DNA  
<213> ARTIFICIAL SEQUENCE

<220>  
<223> KOZAK CONSENSUS SEQUENCE

<220>  
<221> misc\_feature  
<222> (4)..(5)  
<223> n represents a,c,g or t

<400> 94  
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9